

PS Disclosure: Fig 1. 109pp. English.

XX
CC The invention relates to promoter regions from mouse and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy
CC of cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods, can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These
CC substances, e.g. antisense oligonucleotides, transcription factors, or
CC peptide nucleic acids and factors that disrupt signal transduction, are
CC useful for cancer therapy. In particular, gene therapy vectors
CC (especially p67-codapp) comprising the promoter and a viral thymidine
CC kinase gene can be used to convert a product, e.g. gancyclovir, so that
CC telomerase RNA gene through manipulation of transcription factors of
CC effective anticancer therapy and the cloning of the htr gene promoter
CC allows the analysis of therapeutic molecules which modulate htr promoter
CC activity. The present sequence represents a human TR (htr) gene sequence.
XX
SO Sequence 1765 BP; 404 A; 458 C; 480 G; 423 T; 0 other:

Query Match

Best Local Similarity 100.0%; Score 1765; DB 20; Length 1765;
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGGCTGAGACACGAAATCGTTGAACCCGGAGGAGAGTTGCAATG 60
DB 1 AGCTACTCAGAGGCTGAGACACGAAATCGTTGAACCCGGAGGAGAGTTGCAATG 60
QY 61 AGCCGAGATCACGCCACTAGACTCCATCCAGCTGCGGGAAGAACAGAACTCCGTCA 120
DB 61 AGCCGAGATCACGCCACTAGACTCCATCCAGCTGCGGGAAGAACAGAACTCCGTCA 120
QY 121 AAAAAAATGTTTCAATTTATGTTGATTTACTCCCTCTTTTACCTCAACAAACA 180
DB 121 AAAAAAATGTTTCAATTTATGTTGATTTACTCCCTCTTTTACCTCAACAAACA 180
QY 181 CAGCACTACTTTAAAGCAAGTCATGATGAAGCGCTTCTTCTTAATAAAGGAG 240
DB 181 CAGCACTACTTTAAAGCAAGTCATGATGAAGCGCTTCTTCTTAATAAAGGAG 240
QY 241 ATTGAGCTCTTAAGTTAATTAATGATGATTAAGTACCTTGAAGCAATCCCTCTCA 300
DB 241 ATTGAGCTCTTAAGTTAATTAATGATGATTAAGTACCTTGAAGCAATCCCTCTCA 300
QY 301 AGGAAAGCTGAGAGAGCATTTCTAAGGAAAGAGGGGAGGTTGGAATCGAGCATC 360
DB 301 AGGAAAGCTGAGAGAGCATTTCTAAGGAAAGAGGGGAGGTTGGAATCGAGCATC 360
QY 361 CCACTGAGCGAGCAAAATTTCTGTTAGTCAGTCTCCCTGGAATCTATTTTCAAA 420
DB 361 CCACTGAGCGAGCAAAATTTCTGTTAGTCAGTCTCCCTGGAATCTATTTTCAAA 420
QY 421 AGTTTCCAAAAATGTGATGATCAAAACTAGGAATTTGTTCTGTTCTTAAAGCCCTA 480
DB 421 AGTTTCCAAAAATGTGATGATCAAAACTAGGAATTTGTTCTGTTCTTAAAGCCCTA 480
QY 481 AATCTTCTCGTGAATTCATTTTAAAGTAGTCAGAGTGAACGGCGTGTGTGAGAGA 540
DB 481 AATCTTCTCGTGAATTCATTTTAAAGTAGTCAGAGTGAACGGCGTGTGTGAGAGA 540
QY 541 GGAATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTTAAAGAGTGGCAAG 600
DB 541 GGAATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTTAAAGAGTGGCAAG 600
QY 601 TAAAGAGCAAAAGGCTTCCGGAAGTGGGAAAGGCAAGCTCCCTGATGAGCGGGAAG 660
DB 601 TAAAGAGCAAAAGGCTTCCGGAAGTGGGAAAGGCAAGCTCCCTGATGAGCGGGAAG 660
QY 661 ATGGAATTTTATTTCCGTTCCGCCAACACCGCCCGAGAGAGTACTCTCAGAG 720

DB 661 ATGGAATTTTATTTCCGTTCCGCCAACACCGCCCGAGAGAGTACTCTCAGAG 720
QY 721 ACCCGGAGAGTCACTTGTGCAATCCGTGGGCTGGGCGGCGCTCTTTTATTAAGCGA 780
DB 721 ACCCGGAGAGTCACTTGTGCAATCCGTGGGCTGGGCGGCGCTCTTTTATTAAGCGA 780
QY 781 CTGCGCGGAGAGGAGCGGAGGTTGCGAGGTTGAGGCTGGAGAGGAGTGGTGGCAATTTT 840
DB 781 CTGCGCGGAGAGGAGCGGAGGTTGCGAGGTTGAGGCTGGAGAGGAGTGGTGGCAATTTT 840
QY 841 TGTCTAACCTTAAGTGAAGAGGCTAGAGCGCGTCTTTGCTCCCGGCGGTGTTT 900
DB 841 TGTCTAACCTTAAGTGAAGAGGCTAGAGCGCGTCTTTGCTCCCGGCGGTGTTT 900
QY 901 TCTGCTGACTTTCAGGCGGCGGAAAAAGCTTGCGCTGCGGCTTCCACCGTTCAATCTA 960
DB 901 TCTGCTGACTTTCAGGCGGCGGAAAAAGCTTGCGCTGCGGCTTCCACCGTTCAATCTA 960
QY 961 GAGCAAAACAAAAATGTCACTGCTGCGCCCTTCCGCCGGAGACCTGGCGGGGT 1020
DB 961 GAGCAAAACAAAAATGTCACTGCTGCGCCCTTCCGCCGGAGACCTGGCGGGGT 1020
QY 1021 CCGCTGCCAGCGCCCGGAAACCCGCTGAGAGCGCGGTGCGCGGAGGCTTCCGAG 1080
DB 1021 CCGCTGCCAGCGCCCGGAAACCCGCTGAGAGCGCGGTGCGCGGAGGCTTCCGAG 1080
QY 1081 GCACCTACTGCGCACCGCAAGAGTTGCTCTGTCAGCGCGGGTCTCTGCGGGCAAGG 1140
DB 1081 GCACCTACTGCGCACCGCAAGAGTTGCTCTGTCAGCGCGGGTCTCTGCGGGCAAGG 1140
QY 1141 CGAGGTTGAGGCTTTCAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 CGAGGTTGAGGCTTTCAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 GATTCCTGAGCTTGGAGAGTGCACCCAGAGTGGCTGACATGAGTGGCTTTC 1260
DB 1201 GATTCCTGAGCTTGGAGAGTGCACCCAGAGTGGCTGACATGAGTGGCTTTC 1260
QY 1261 TGTGTTGAGGAG 1320
DB 1261 TGTGTTGAGGAG 1320
QY 1321 GTGAAGCCCAAACTGACTGACTGAGGCGAGTGTCTGCAATTTGAGAGAGAGAGAG 1380
DB 1321 GTGAAGCCCAAACTGACTGACTGAGGCGAGTGTCTGCAATTTGAGAGAGAGAGAG 1380
QY 1381 GCACTTCCAAAGTGGCCAAATGATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 GCACTTCCAAAGTGGCCAAATGATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 TGGGTTGAGGAG 1500
DB 1441 TGGGTTGAGGAG 1500
QY 1501 TCTGCTGCTGAGATTTTGTGAGGTTTGTGCTTCCCAAGTGAATCTGACAGCATC 1560
DB 1501 TCTGCTGCTGAGATTTTGTGAGGTTTGTGCTTCCCAAGTGAATCTGACAGCATC 1560
QY 1561 CCTCAAGGAGGAG 1620
DB 1561 CCTCAAGGAGGAG 1620
QY 1621 ATATTATTAATGAAGATCTAAATGAACATTTGAAATTTGTTTAAATGATGATGAT 1680
DB 1621 ATATTATTAATGAAGATCTAAATGAACATTTGAAATTTGTTTAAATGATGATGAT 1680
QY 1681 TTAAGCAGAGAGTTAGAGATTTCTTTTGAAGAAATTAAGCTTGGAGATGACCTGAGC 1740
DB 1681 TTAAGCAGAGAGTTAGAGATTTCTTTTGAAGAAATTAAGCTTGGAGATGACCTGAGC 1740
QY 1741 AGTAGATATTAACCCCAAGGTT 1765

DB	1741	AGTAGCATATATACCCCAAGGCT	1765
RESULT	2		
ID	AAV22994		
XX	AAV22994	standard; DNA; 2426 BP.	
XX	AAV22994:		
XX	30-JUL-1998	(first entry)	
DE	DNA containing human telomerase RNA component gene sequences.		
XX			
KW	Human; telomerase RNA component gene sequence;		
KW	ribonucleoprotein enzyme; cancer cell; telomerase activity;		
KW	reporter construct; transcription regulatory region;		
KW	prophylaxis; therapy; telomerase-related condition;		
XX	chromatin position effect; ss.		
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	TATA_signal	1438..1444	
FT		/*tag- a	
FT	misc_feature	1238..1259	
FT		/*tag- b	
FT	misc_feature	/note= "PSE consensus sequence"	
FT		1406..1414	
FT		/*tag- c	
FT	CAAT_signal	/note= "PSE consensus sequence"	
FT		1399..1406	
FT		/*tag- d	
FT	misc_feature	1354..1359	
FT		/*tag- e	
FT	misc_feature	/note= "SP1 consensus sequence"	
FT		1234..1245	
FT		/*tag- f	
FT		/note= "beta-Interferon response element"	
XX			
PN	W09811207-A2.		
XX			
PD	19-MAR-1998.		
XX			
PP	16-SEP-1997;	97MO-US16450.	
XX			
PR	16-SEP-1996;	96US-0714482.	
XX			
PA	(GERO-) GERON CORP.		
XX			
PI	Harley C, Villeponteau B;		
XX			
DR	WPI: 1998-207376/18.		
XX			
PT	Human telomerase reporter constructs - useful in assays for		
PT	regulators of mammalian telomerase expression		
XX			
PS	Claim 6; Pages 27-28; 59pp; English.		
CC	The present sequence contains human telomerase RNA component gene		
CC	sequences. Telomerase is a ribonucleoprotein enzyme that synthesises		
CC	one strand of the telomeric DNA using as a template a sequence contained		
CC	within the RNA component of the enzyme. Most cancer cells express high		
CC	levels of telomerase activity, while in normal somatic human cells,		
CC	telomerase is not detected. The specification describes the production		
CC	of a telomerase reporter construct which comprises a recombinant		
CC	polynucleotide having a transcription regulatory region of a telomerase		
CC	gene operably linked to a nucleotide sequence encoding a reporter		
CC	polynucleotide heterologous to the transcription regulatory region.		
CC	Expression of the reporter polynucleotide is detectable. The telomerase		
CC	reporter construct is used in screening assays for determining modulators		
CC	of transcription. The modulators can be used for prophylaxis or therapy		
CC	of telomerase-related conditions. The reporter construct which has a		
CC	selectable drug marker can be used to generate position effect reporter		

Query Match	97.4%	Score 1719.6	DB 19	Length 2426
Best Local Similarity	99.1%	Pred. No. 0	Mismatches 14	Indels 2
Matches 1750	Conservative	0		
OY	1	AGCTCTCAGGAGGGGTGAGACACAGAAATCGCTTGAACCCGGGAGGACAGAGTTCGAGNG	60	
Db	662	AGCTACTCAGGAGGCTGACACACAGAAATCGCTTGAACCCGGGAGGACAGAGTTCGAGNG	720	
OY	61	AGCCGAGATCACAGCCACTAGACTCCATCCAGCCTGGGCGCAAGAGACAGACTCCGTCTCA	120	
Db	721	AGCCGAGATCACAGCCACTAGACTCCATCCAGCCTGGGCGCAAGAGACAGACTCCGTCTCA	780	
OY	121	AAAAAAAAAATCGTTACAAATTTATGCTGATTTACTCCCTCTTTTAACTCATCAAGACA	180	
Db	781	AAAAAAAAAATCGTTACAAATTTATGCTGATTTACTCCCTCTTTTAACTCATCAAGACA	840	
OY	181	CAGCACTACTTTAAAGCAAGTCATGATTTGAAGCCCTTCTTCTTAATAAAGGGAG	240	
Db	841	CAGCACTACTTTAAAGCAAGTCATGATTTGAAGCCCTTCTTCTTAATAAAGGGAG	900	
OY	241	ATTTCAGTCCCTTAAGATTAAATGATGATGATACACTTGATTTAAAGCATTCTCTCTCA	300	
Db	901	ATTTCAGTCCCTTAAGATTAAATGATGATGATACACTTGATTTAAAGCATTCTCTCTCA	960	
OY	301	AGGAGAGCTGAGAGAGGCATTCTAAGGAAAAAGGGGACAGGTTGGAACTCGAGCATTC	360	
Db	961	AGGAGAGCTGAGAGAGGCATTCTAAGGAAAAAGGGGACAGGTTGGAACTCGAGCATTC	1020	
OY	361	CCACAGAGCCGAGACAAGATTCTGCTGTAGTACAGTCTCCCTGGGAAATCTATTTTCACAA	420	
Db	1021	CCACAGAGCCGAGACAAGATTCTGCTGTAGTACAGTCTCCCTGGGAAATCTATTTTCACAA	1080	
OY	421	AGTTTCTCCAAAAAATGATGATCAAAATCTAGGAATTTAGTTCTGTCTTAAGGCCCTA	480	
Db	1081	AGTTTCTCCAAAAAATGATGATCAAAATCTAGGAATTTAGTTCTGTCTTAAGGCCCTA	1140	
OY	481	AAATCTTCTCTGTAATTCATTTTTAAAGTAGTCGAGGTGAACCCGCGTGTGCTGACAGA	540	
Db	1141	AAATCTTCTCTGTAATTCATTTTTAAAGTAGTCGAGGTGAACCCGCGTGTGCTGACAGA	1200	
OY	541	GGATGAAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAGSTCGGAAG	600	
Db	1201	GGATGAAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAGSTCGGAAG	1260	
OY	601	TAAAGACGCAAAAGCCTTTCCGGAGGTGGGGAAGGGCAACGTCCTTCATATGGCCGGAA	660	
Db	1261	TAAAGACGCAAAAGCCTTTCCGGAGGTGGGGAAGGGCAACGTCCTTCATATGGCCGGAA	1320	
OY	661	ATGGAACCTTTAATTTCCCGTTCGCCCAACACAGCCGCCCGAGAGAGTACTCTCACGAG	720	
Db	1321	ATGGAACCTTTAATTTCCCGTTCGCCCAACACAGCCGCCCGAGAGAGTACTCTCACGAG	1380	
OY	721	AGCCGAGAGATCAGCTTGGCCAATTCGTGCGGTGGCGCGCTCCCTTTATAGCCGA	780	
Db	1381	AGCCGAGAGATCAGCTTGGCCAATTCGTGCGGTGGCGCGCTCCCTTTATAGCCGA	1440	
OY	781	CTCGCCCGGACACGACCGGGTTGGGGAAGGGGCGCTGGAAGGGGTGGGTGGCCATTTTT	840	
Db	1441	CTCGCCCGGACACGACCGGGTTGGGGAAGGGGCGCTGGAAGGGGTGGGTGGCCATTTTT	1500	
OY	841	TGTCTTAACCTTAAGTAGAAGAGGCGTAGCGCGCTTTTCTCTCCCGCGGCTGTGTTT	900	
Db	1501	TGTCTTAACCTTAAGTAGAAGAGGCGTAGCGCGCTTTTCTCTCCCGCGGCTGTGTTT	1560	
OY	901	TCTGCTGACTTTCAAGCGGGCGAAAAAGCCTGCGCCTGCGCCTTCACCTTCATTCTTA	960	
Db		TCTGCTGACTTTCAAGCGGGCGAAAAAGCCTGCGCCTGCGCCTTCACCTTCATTCTTA		


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Oy 421 AGTTCTCAAAAAATGTGATCAAAAGTAGAATTAAGTTCGTGTCTTAGGCCCTA 480
    |||||||
Db 1081 AGTTCTCAAAAAATGTGATCAAAAGTAGAATTAAGTTCGTGTCTTAGGCCCTA 1140
Oy 481 AATCTTCCTGTGAATTCATTTTAAAGTAGTCGAGGTGAACGGCTGTCTGTCAGA 540
    |||||||
Db 1141 AATCTTCCTGTGAATTCATTTTAAAGTAGTCGAGGTGAACGGCTGTCTGTCAGA 1200
Oy 541 GGTATAGAAAAAGGCGCTGTGATACCTCAAGTATAGTTTACCTTTAAAGAGTCCGAAG 600
    |||||||
Db 1201 GGTATAGAAAAAGGCGCTGTGATACCTCAAGTATAGTTTACCTTTAAAGAGTCCGAAG 1260
Oy 601 TAAAGACGAAAGCCCTTTCGCGAGCTGCGGAAGGCAACGTCCTTCTCATGAGCGGAA 660
    |||||||
Db 1261 TAAAGACGAAAGCCCTTTCGCGAGCTGCGGAAGGCAACGTCCTTCTCATGAGCGGAA 1320
Oy 661 ATGGAACTTTAATTTCCGCTTCCCGCAACCAAGCCCGCGAGAGAGTACTCTACGAG 720
    |||||||
Db 1321 ATGGAACTTTAATTTCCGCTTCCCGCAACCAAGCCCGCGAGAGAGTACTCTACGAG 1380
Oy 721 AGCCGCGAGAGTACGTTGGCCCAATCCGTGCGGTGGCGGCGCTCCCTTTATAAGCCGA 780
    |||||||
Db 1381 AGCCGCGAGAGTACGTTGGCCCAATCCGTGCGGTGGCGGCGCTCCCTTTATAAGCCGA 1440
Oy 781 CTCGCCCGGACGCGACCGGGTTTC---GAGGGTGGGCTGGAGAGGGTGGGCGCAT 836
    |||||||
Db 1441 CTCGCCCGGACGCGACCGGGTTGGGAGGAGGAGGGTGGGCGCTGGAGGGTGGGCGCAT 1500
Oy 837 TTTTCTCTAACCTTAAGTCAGAGAGGGCGTAGCGCCGTTCCTTTCCTCCCGCGCTG 896
    |||||||
Db 1501 TTTTCTCTAACCTTAAGTCAGAGAGGGCGTAGCGCCGTTCCTCCCGCGCGCTG 1560
Oy 897 TTTTCTCTGACTTTCAGCGCGGGGAAAAAGCTGCGGCTGGCGGCTTCACACCTTCAT 956
    |||||||
Db 1561 TTTTCTCTGACTTTCAGCGCGGGGAAAAAGCTGCGGCTGGCGGCTTCACACCTTCAT 1620
Oy 957 TCTAGAGCAAAACAAAAATATCTAGCTGTGCGCCGCTCCCGCTCCGGGAGACTCGCGC 1016
    |||||||
Db 1621 TCTAGAGCAAAACAAAAATATCTAGCTGTGCGCCGCTCCCGCTCCCGC-66GACCTCGGC 1679
Oy 1017 GGGTGGCTGCCAGCGCCCGCAACCCCGCTGAGAGCGCGCGGTGGCGGCGCTTCCTC 1076
    |||||||
Db 1680 GGGTGC-CTGGCCAGCCCGCAACCCCGCTGAGAGCGCGCGGTGC-CCGGGCGCTTCCTC 1137
Oy 1077 GGAGGCACTTACTGGCAGCGCGGAAGGT-GGCTCTGTAGCGCGCGGCTCTCGGGGGC 1135
    |||||||
Db 1738 GGAGGCACTTACTGGCAGCGCGGAAGGTGGCTCTGTAGCGCGCGGCTCTCGGGGGC 1197
Oy 1136 GAGGGGAGGTTTCAGGCTTTAGCGCGAGAGAGAGAGAGGAGGAGTCCCGCGCGC 1195
    |||||||
Db 1798 GAGGGGAGGTTTC-CCGTTTCAAGCGCGCAGAGAGAGAGAGGAGGAGT-CCCGCGCGC 1855
Oy 1196 GGGCGAATTCCTGAGCTGTGGAGCTGCACCCAGAGACTCGGCTCAACATGCAATTCGC 1255
    |||||||
Db 1856 GGGCGAATTCCTGAGCTGTGGAGCTGCACCCAGAGACTCGGCTCAACATGCAATTCGC 1915
Oy 1256 TTTTCTGTGGTGGGGGGAAGCGGATTCGTGCGCATCCCTACCCCTCCCGGCAATGGG 1315
    |||||||
Db 1916 TTTTCTGTGGTGGGGGGAAGCGGATTCGTGCGCATCCCTACCCCTCCCGGCAATGGG 1975
Oy 1316 GGGTGTGAACCCCAAAACCTGACTGAGGCGAGTGTGTCAAAATTGAGAGAGAGC 1375
    |||||||
Db 1976 GGGTGTGAACCCCAAAACCTGACTGAGGCGAGTGTGTCAAAATTGAGAGAGAGC 2035
Oy 1376 TGAAGCACTTCCAAAGTGGGCCAAATGAGGAGTGAAGCGGGGTTCCCTGAGGC 1435
    |||||||
Db 2036 TGAAGCACTTCCAAAGTGGGCCAAATGAGGAGTGAAGCGGGGTTCCCTGAGGC 2095
Oy 1436 GTTTCCTGCGTGGTCTTCCCGCTTTCCTGCTTTTGTGCTTTATGTTGTATTCACAC 1495
    |||||||
Db 2096 GTTTCCTGCGTGGTCTTCCCGCTTTCCTGCTTTTATGTTGTATTCACAC 2155
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Oy 1496 TTAGTCTGCTCTGACAGATTTTGTGAGGTTTTGCTTCTCCCAAGTAGATCTGACC 1555
    |||||||
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Oy 1556 AGTCCCTCAACGGGCTGTGGGAGAACAGTCATTTTTTTTTTGAGAGATCATTTAACATT 1615
    |||||||
Db 2216 AGTCCCTCAACGGGCTGTGGGAGAACAGTCATTTTTTTTTTGAGAGATCATTTAACATT 2275
Oy 1616 AATGAATTTTATTTAGAGATCTAATGAACATTCGAATTCGTTCCTTAAATGTCGA 1675
    |||||||
Db 2276 AATGAATTTTATTTAGAGATCTAATGAACATTCGAATTCGTTCCTTAAATGTCGA 2335
Oy 1676 TCGGTTTATGCCAGAGTTAGAGTTTCTTTTGAATAATTAGACCTTGGCGATGACCT 1735
    |||||||
Db 2336 TCGGTTTATGCCAGAGTTAGAGTTTCTTTTGAATAATTAGACCTTGGCGATGACCT 2395
Oy 1736 TGAAGATGAGATATTAACCCCAAGCTT 1765
    |||||||
Db 2396 TGAAGATGAGATATTAACCCCAAGCTT 2425

RESULT 4
AAT11027
ID AAT11027 standard; DNA; 2425 BP.
XX
XX AAT11027;
AC
XX
XX
DT 09-JUN-1996 (first entry)
XX
DE DNA encoding the human telomerase RNA component.
XX
XX Telomerase; mammal; antisense; triplex forming oligonucleotide;
KW plasmid; probe; primer; ribozyme; ss.
XX
XX Homo sapiens.
OS
XX
XX W09601614-A2.
PN
XX
XX 25-JAN-1996.
PD
XX
XX 07-JUL-1995; 95WO-US08620.
PF
XX
XX 07-JUN-1995; 95US-0485778.
PR 07-JUL-1994; 94US-0272102.
PR 27-OCT-1994; 94US-0330123.
PR 13-FEB-1995; 95US-0387524.
XX
XX (GOLD-) COLD SPRING HARBOR LAB.
PA
XX
XX Andrews WH, Avillon AH, Feng J, Funk W, Greider C;
PI Maruenda MA, Villeponteau B;
XX
XX WPI: 1996-097428/10.
XX
XX RNA components of (non)human mammalian telomerase(s) - useful in
PT studying cell senescence and immortalisation
XX
XX Claim 37; Figure 1; 85pp; English.
PS
XX
XX The RNA components of (non) human mammalian telomerase(s) especially
CC from mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the
CC telomerase; probes and primers can be used in detection; vectors and
CC host cells transformed with the isolated telomerase genes can be
CC used for production of telomerases; RNA and DNA ribozymes and triplex
CC forming oligonucleotides directed against the telomerase genes can
CC be used therapeutically as can plasmids. A mouse which lacks the
CC telomerase gene (also claimed) can be used for study of telomere
CC regulation in vivo, and the role it plays in immortalisation. This
CC DNA sequence encodes the human telomerase RNA component.
XX
XX Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 other;
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QY 1017 GGGTGCCTCCCCAGCCCCCGCCCTGGAGGCGCGGTGCGGCCGGGGCTTCGC 1076
|||||
Db 1680 GGGTCG-CTGCCCCAGCCCCCGCCCTGGAGGCGCGGTGCGG-CCGGGCTTCGC 1737

QY	1017	GGAGTCCCTGCGCCACACCCCGACACCCCGCGGAGAGGCGCGGCTGGCCCGCGGGAGCTTCTCC	1076		
Db	1680	GGGTGC -CTGCCACACCCCGACACCCCGCTGGAGGCGCGGTCG -CCGGGCTTCTCC	1737		
QY	1077	GGAGCACCTACTGCGCACCGGGAAGTT -GGCTCTGTACGCCGCGGCTCTCTCGGGGCG	1135		
Db	1738	GGAGGACACCAATCGCCACCGGAGAGATTGGCTCTGTACGCCGCGGCTCTCGGGGCG	1797		
QY	1136	GAGGGCGAGGTTCAAGGCGTTTCAGCGCCGAGAAAGAGAACGAGAGTCCCGCGCGC	1195		
Db	1798	GAGGGCGAGGTTCA -CGTTTCAGGCGCGAGAAAGAGAACGAGAGT -CCCGCGCGC	1855		
QY	1196	GGCGGATTCCTCGAGCTGTGGAGCTGCACCCAGAGACTCGGCTCACACATGCACTTCTGC	1255		
Db	1856	GGCGGATTCCTCGAGCTGTGGAGCTGCACCCAGAGACTCGGCTCACACATGCACTTCTGC	1915		
QY	1256	TTTCTCTGTGTGGGGGGAGACCCGATCGTGGCATCCGTCAACCCCTCGCGGCACTGGG	1315		
Db	1916	TTTTCTGTGTGTGGGGGGAGACCCGATCGTGGCATCCGTCAACCCCTCGCGGCACTGGG	1975		
QY	1316	GGCTGTGAACCCCCCAACCTGACTGCTGGGCGAGTGTGCGCAATTTGGCAGAGACG	1375		
Db	1976	GGCTGTGTGAACCCCCCAACCTGACTGCTGGGCGAGTGTGCGCAATTTGGCAGAGACG	2035		
QY	1376	TGAGGCACTCTCCAAAGTCGGCCAAAATGAAATGGCAGTGAACCGGGTTGCTGAGACC	1435		
Db	2036	TGAAAGCACTCTCCAAAGTCGGCCAAAATGAAATGGCAGTGAACCGGGTTGCTGAGACC	2095		
QY	1436	GTTCCTGGTGGGGTTCGCCGCTCCGCTTTTGTGTGCTTTTATGTTGATTTAAC	1495		
Db	2096	GTTCCTGGTGGGGTTCGCCGCTCCGCTTTTGTGTGCTTTTATGTTGATTTAAC	2155		
QY	1496	TTAGTTCCTGCTGCAAGATTTTGTGAGTTTGTGTCTCCCAAGGTAGATCTGCACC	1555		
Db	2156	TTAGTTCCTGCTGCAAGATTTTGTGAGTTTGTGTCTCCCAAGGTAGATCTGCACC	2215		
QY	1556	AGTCCCTCAACGGGGGTGGGAGACACTATTTTTTTTGTGAGAGATCATTTAACATTT	1615		
Db	2216	AGTCCCTCAACGGGGGTGGGAGACACTATTTTTTTTGTGAGAGATCATTTAACATTT	2275		
QY	1616	AATGAATATTTAATTAGAGATCTAAATGAACATTTGGAATTTGTTCCTTAATGTCA	1675		
Db	2276	AATGAATATTTAATTAGAGATCTAAATGAACATTTGGAATTTGTTCCTTAATGTCA	2335		
QY	1676	TCGGTTATTCGACAGAGTTTGAAGTTCTTTTTTGAATAATTTAGACCTGGCGATGACT	1735		
Db	2336	TCGGTTATTCGACAGAGTTTGAAGTTCTTTTTTGAATAATTTAGACCTGGCGATGACT	2395		
QY	1736	TGAGCAGTAGGATATAACCCCAACAGTT 1765			
Db	2396	TGAGCAGTAGGATATAACCCCAACAGTT 2425			
RESULT 5					
AAV41194	AAV41194 standard; DNA; 981 BP.				
XX	AAV41194:				
XX	08-OCT-1998	(first entry)			
DE	PsiI fragment containing RNA component of human telomerase (hTR).				
XX					
KW	RNA component; bladder cancer; antisense oligonucleotide; infection;				
KW	neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;				
KW	contraception; sterilisation; immunosuppression; therapeutic; hTR;				
KW	immune system down-regulation; anti-inflammatory therapy; ss.				
XX	Homo sapiens.				
OS					
XX					
Key	Location/Qualifiers				
TF	misc feature 266..736				

PD 19-MAR-1998.
 XX
 PF 13-SEP-1996; 96WO-US14679.
 XX
 PR 13-SEP-1996; 96WO-US14679.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Adams RR, Andrews WH, Feng J, Villeponteau B;
 XX
 DR WPI: 1998-207373/18.
 XX
 PT Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
 XX telomerase activity
 PS
 XX Disclosure: Fig 9A-B; 86pp; English.

This nucleotide sequence comprises an approximately 1 kb PstI restriction fragment of plasmid pGRN33 that includes the human telomerase hTR gene. hTR3 mRNA levels correlate with telomerase activity levels in a variety of mortal and immortal cell lines. In methods of the invention, measurements of telomere length, telomerase activity or hTR levels can be used to identify immortal cells, such as cancer cells, and to evaluate the proliferative capacity of the cell. Gene therapy vectors encode useful nucleic acids, such as hTR, or antisense nucleic acids or ribozymes that target TPC2, TPC3 (see AAV19479-80) and/or hTR gene products.

Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other;

Query Match 54.8%; Score 967.4; DB 19; Length 981;
 Best Local Similarity 99.8%; Pred. No. 1,3e-261;
 Matches 979; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 534 CTGCAGAGATAGAAAAAGCCCTGTGATACCTGATAGTTTCACTTTAAAGAG 593
 DB 1 CTGCAGAGATAGAAAAAGCCCTGTGATACCTGATAGTTTCACTTTAAAGAG 60
 QY 594 TCGGAAGTAAAGCGCAAAAGCTTTCCGAGCTGGGGAAGGGCAACGTCCTTCATG 653
 DB 61 TCGGAAGTAAAGCGCAAAAGCTTTCCGAGCTGGGGAAGGGCAACGTCCTTCATG 120
 QY 654 GCCGGAATGAACTTAAATTCCTGTCGCCCAACAGCCCGCGGAGAGAGTACTG 713
 DB 121 GCCGGAATGAACTTAAATTCCTGTCGCCCAACAGCCCGCGGAGAGAGTACTG 180
 QY 714 TCAAGAGAGCGGAGAGTACCTTGCCCAATCCGTGCGGCGCTCCCTTAT 773
 DB 181 TCAAGAGAGCGGAGAGTACCTTGCCCAATCCGTGCGGCGCTCCCTTAT 240
 QY 774 AAGCCGACTCGCCGCGACGACCGGTTGGGAGAGGGGCTGGAGGGGTGTGGC 833
 DB 241 AAGCCGACTCGCCGCGACGACCGGTTGGGAGAGGGGCTGGAGGGGTGTGGC 300
 QY 834 CATTCTTTGTCAACCTTACTAGAGGGCGTAGCGCGCGCTTGTTCCTCCGCG 893
 DB 301 CATTCTTTGTCAACCTTACTAGAGGGCGTAGCGCGCGCTTGTTCCTCCGCG 360
 QY 894 CTGTTTTCTCGCTGACTTTCAGCGGGGGAAGAGCTTCGCGCTTCACCGTT 953
 DB 361 CTGTTTTCTCGCTGACTTTCAGCGGGGGAAGAGCTTCGCGCTTCACCGTT 420
 QY 954 CATTCTAGAGCAAAAAAATGTACGTGCTGCGCGCTTCGCGGGGAGCTGC 1013
 DB 421 CATTCTAGAGCAAAAAAATGTACGTGCTGCGCGCTTCGCGGGGAGCTGC 480
 QY 1014 GCGGGTGGCGGCGCCGACCGCCGACCGCGCTGAGAGCGCGGTGGCGCGGCTTC 1073
 DB 481 GCGGGTGGCGGCGCCGACCGCCGACCGCGCTGAGAGCGCGGTGGCGCGGCTTC 540
 QY 1074 TCCGAGGACCTACTGCGACCGGAGAGATT-GGCTGTGACCGCGGCTCTCTGGG 1132
 DB 541 TCCGAGGACCTACTGCGACCGGAGAGATTGGGCTCTGTGACCGCGGCTCTCTGGG 600

QY 1133 GCGGAGGCGAGTTTCAGGCTTTCAAGCCCGCAGAGAAAGAGAGCGAGTCCCGCG 1192
 DB 601 GCGGAGGCGAGTTTCAGGCTTTCAAGCCCGCAGAGAAAGAGAGCGAGTCCCGCG 660
 QY 1193 CGCGGCGGATTCCTGAGCTGTGGACGTGACCCAGAGACTGCGTCAACATGAGTT 1252
 DB 661 CGCGGCGGATTCCTGAGCTGTGGACGTGACCCAGAGACTGCGTCAACATGAGTT 720
 QY 1253 CGCTTCCTGTTGTGGGGGGAAGCGCGATGTGCGCATCCGTACCCCTCGCGGAGT 1312
 DB 721 CGCTTCCTGTTGTGGGGGGAAGCGCGATGTGCGCATCCGTACCCCTCGCGGAGT 780
 QY 1313 GGGGGCTTGTGAACCCCAAACTGACTAGGCGGCAATGTGCTGCAATTTGCGAGAG 1372
 DB 781 GGGGGCTTGTGAACCCCAAACTGACTAGGCGGCAATGTGCTGCAATTTGCGAGAG 840
 QY 1373 ACCTGAAGCACCCTCCAAAGTGGCCAAATGATGGCAGTGGCGGTTGCTGGA 1432
 DB 841 ACCTGAAGCACCCTCCAAAGTGGCCAAATGATGGCAGTGGCGGTTGCTGGA 900
 QY 1433 GCGGTCGTGCGGGGTTCTCCGCTTCCGCTTTTGTGCTTTAAVGGTTGTATTAC 1492
 DB 901 GCGGTCGTGCGGGGTTCTCCGCTTCCGCTTTTGTGCTTTAAVGGTTGTATTAC 960
 QY 1493 AACTTAGTTCCTGCTGTGCAG 1513
 DB 961 AACTTAGTTCCTGCTGTGCAG 981

RESULT 7
 AAD24234
 ID AAD24234 standard; DNA: 981 BP.

XX AAD24234;

XX 07-MAR-2002 (first entry)

XX Human telomerase (hTR) gene.

XX Human; telomerase; TR; telomerase activity-related disease; therapy;

XX cancer; pregnancy; fertility; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT msc_feature 267..715

FT /note="hTR transcript serves as template in the telomerase ribonucleoprotein"

PN US6300110-B1.

PD 09-OCT-2001.

PF 23-DEC-1998; 98US-0220157.

PR 09-SEP-1995; 95US-003492P.

PR 13-SEP-1996; 96US-0710249.

PR 05-JAN-1996; 96US-0583808.

XX (GERO-) GERON CORP.

XX Villeponteau B, Feng J, Andrews WH, Adams RR;

XX WPI: 2002-033174/04.

PT Peptide products of the human TPC2 and TPC3 gene are involved in
 PT regulation of telomere length and activity are useful to diagnose and
 PT treat telomere length and activity-related diseases -
 XX Example: Fig 9; 60pp; English.

CC The invention relates to methods and reagents for regulating telomere
CC length and for modulating telomerase activity in mammalian cells. The
CC invention also relates to purified, synthetic or recombinant peptides
CC such as TPC2 or TPC3 used for detecting regulators of telomere length
CC and telomerase activity in mammalian cells and for a variety of related
CC diagnostic and therapeutic purposes. The method is useful for screening,
CC diagnosing, monitoring and treating diseases and other conditions such as
CC cancer, pregnancy, fertility, telomere length and telomerase-activity.
CC The present sequence is human telomerase (hTR) gene.
XX

Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.8%; Score 966.4; DB 24; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.5e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTACTTTCACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTACTTTCACCTTTAAAGAGG 60
QY 594 TCGGAAGTAAAGACGCAAGCCCTTCCGAGGTGGGAAGGCAAGCTTCCTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCCTTCCGAGGTGGGAAGGCAAGCTTCCTCATG 120
QY 654 GCCGAAATGAACTTTATTTCCCGTTCCCCCAACAGCCGCCGCGAGAGAGTACTC 713
DB 121 GCCGAAATGAACTTTATTTCCCGTTCCCCCAACAGCCGCCGCGAGAGAGTACTC 180
QY 714 TCACGAGACCCGCGAGAGTACCTTGCCCAATCCGTGCGGCGCGCTCCCTTAT 773
DB 181 TCACGAGACCCGCGAGAGTACCTTGCCCAATCCGTGCGGCGCGCTCCCTTAT 240
QY 774 AAGCGAGTCCGCGGACGACGCGGTTGGGAGAGGTGGGAGGGGTGGTGGC 833
DB 241 AAGCGAGTCCGCGGACGACGCGGTTGGGAGAGGTGGGAGGGGTGGTGGC 300
QY 834 CATTTTGTCTAACCTTACTAGAGAGGCGTAGCGCGCTTTTCTCCCGCGG 893
DB 301 CATTTTGTCTAACCTTACTAGAGAGGCGTAGCGCGCTTTTCTCCCGCGG 360
QY 894 CGTTTTTTCCTGACTTTCAAGCGGGGGAAGGCTTGGCGCTGCGCTTCCACCGTT 953
DB 361 CGTTTTTTCCTGACTTTCAAGCGGGGGAAGGCTTGGCGCTGCGCTTCCACCGTT 420
QY 954 CATTTAGAGCAAAATAATGTGAGTGTGGCCGCTTCCCGGCGGACCTGC 1013
DB 421 CATTTAGAGCAAAATAATGTGAGTGTGGCCGCTTCCCGGCGGACCTGC 480
QY 1014 GCGGGGTGCGTGGCCAGCCCGGAACCCGCTGAGGCGCGGTGGCGCGGCGCTTC 1073
DB 481 GCGGGGTGCGTGGCCAGCCCGGAACCCGCTGAGGCGCGGTGGCGCGGCGCTTC 540
QY 1074 TCCGAGAGCACTACTGCCACCGCGAAGT- GCGTCTGTACGCCGCGGTCTTCGCG 1132
DB 541 TCCGAGAGCACTACTGCCACCGCGAAGT- GCGTCTGTGTAGCGCGGCTCTCGGG 600
QY 1133 GCGGAGGGGAGGTTTTCAGGCGCGGAGGAAGGAGGAGGAGGAGGCGCGG 1192
DB 601 GCGGAGGGGAGGTTTTCAGGCGCGGAGGAAGGAGGAGGAGGAGGAGGCGCGG 660
QY 1193 GCGGAGGCACTTCCGTGAGCTGTGGAGCTGCACCGAGACTCGGCTCAGATG 1252
DB 661 GCGGAGGCACTTCCGTGAGCTGTGGAGCTGCACCGAGACTCGGCTCAGATG 720
QY 1253 CGCTTTCCTGTTGGTGGGGGAACCGCGATCGTCCCATTCCTGCGCGGCACT 1312
DB 721 CGCTTTCCTGTTGGTGGGGGAACCGCGATCGTCCCATTCCTGCGCGGCACT 780
QY 1313 GGGGAGCTTGGAACCCCAAAACCTGACTAGTGGGCGCAATGTGCTCAATTGGCAGAG 1372
DB 781 GGGGAGCTTGGAACCCCAAAACCTGACTAGTGGGCGCAATGTGCTCAATTGGCAGAG 840
QY 1373 AGGTGAAGCACCTCCAAAGTGGGCCAAATGATGGGCAGTGAGCGGCGTTGCCGTGA 1432

DB 841 ACGTGAAGCACCTCCAAAGTCGGCCAAATGATGAGCGAGTGAGCGGGGTGCTGGA 900
QY 1433 GCCGTTCTCGCTGGGTGTCTCCGCTTCCGCTTTTGTGCTTTATGCTGTATTC 1492
DB 901 GCCGTTCTCGCTGGGTGTCTCCGCTTCCGCTTTTGTGCTTTATGCTGTATTC 960
QY 1493 AACTTGTCTCGCTGTGCAG 1513
DB 961 AACTTGTCTCGCTGTGCAG 981

RESULT 8
AAT89242
ID AAT89242 standard; DNA; 981 BP.
XX
AC AAT89242;
XX
DT 12-MAY-1998 (first entry)
XX
DE Clone containing hTR sequence.
XX
KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW inhibitor; human telomerase RNA; hTR; ds.
XX
OS Synthetic.
XX
FH Homo sapiens.
FH
FT Key Location/Qualifiers
FT misc_difference 265..716
FT /*tag= a
FT /*note= "human telomerase RNA"
XX
PN W09738013-A1.
XX
XX 16-OCT-1997.
XX PD
XX 09-APR-1997; 97MO-US05931.
XX PF
XX 09-APR-1996; 96US-0630019.
XX PR
XX (GERO-) GERON CORP.
XX PA
XX Corey D, Norton JC, Platyszek MA, Shay JW, Wright WE;
XX
XX WPI: 1997-512647/47.
XX DR
XX
XX PT New peptide nucleic acids hybridising to mammalian telomerase RNA -
XX PT used to inhibit telomerase, for treating tumours and other
XX PT proliferative diseases, also for diagnosis
XX
XX PS Disclosure: Pages 20-21; 76pp; English.
XX
XX This fragment of cloned DNA contains the human telomerase RNA (hTR)
XX CC sequence, (266-716bp). The hTR region contains a CCC template which
XX CC the peptide nucleic acid (PNA) can recognise. The presence of a GGG
XX CC in the PNAs allows for the specific hybridisation to the template
XX CC region of this hTR component. PNAs can be used as probes to detect the
XX CC RNA component of mammalian telomerase and as inhibitors of telomerase
XX CC activity, especially in the treatment of cancer.
XX
SO Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.7%; Score 965.8; DB 18; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.6e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTACTTTCACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTACTTTCACCTTTAAAGAGG 60
QY 594 TCGGAAGTAAAGACGCAAGCCCTTCCGAGGTGGGAAGGCAAGCTTCCTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCCTTCCGAGGTGGGAAGGCAAGCTTCCTCATG 120

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Db      61  TCGGAAGTAAGACGCAAAAGCCTTCCCGGAGCTGCGGAGGCAACGCTCCTCTCATG 120
Oy      654  GCCGGAATGGAACCTTATTTCCCGTTCCCGCCACACGCGCCGAGAGAGTACTC 713
Db      121  GCCGGAATGGAACCTTATTTCCCGTTCCCGCCACACGCGCCGAGAGAGTACTC 180
Oy      714  TCACGAGAGCGCGAGAGTACAGTGGGCAATCCGTCGGTGGGCGCGCTCCCTTAT 773
Db      181  TCACGAGAGCGCGAGAGTACAGTGGGCAATCCGTCGGTGGGCGCGCTCCCTTAT 240
Oy      774  AAGCGGATCCCGCGCGACCGCGGTCGCGAGGGTGGGCTGGAGAGGGTGTGTC 833
Db      241  AAGCGGATCCCGCGCGACCGCGGTCGCGAGGGTGGGCTGGAGAGGGTGTGTC 300
Oy      834  CATTTTGTCTAACCCCTAACCTAGAGAGGGGTAGGGGCGCTGCTTTTGGTCCCGCG 893
Db      301  CATTTTGTCTAACCCCTAACCTAGAGAGGGGTAGGGGCGCTGCTTTTGGTCCCGCG 360
Oy      894  CTGTTTTCTGCGTACTTTTCAGCGGGCGGAAAGCCCTGCGCGCTTCCACCGTT 953
Db      361  CTGTTTTCTGCGTACTTTTCAGCGGGCGGAAAGCCCTGCGCGCTTCCACCGTT 420
Oy      954  CATTTAGAGCAACAAATAATGTCAGTGTGCTGCGCGCTTCCCGCGGAGCTTC 1013
Db      421  CATTTAGAGCAACAAATAATGTCAGTGTGCTGCGCGCTTCCCGCGGAGCTTC 480
Oy      1014  GCGGGGTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1073
Db      481  GCGGGGTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Oy      1074  TCGGAGAGCACTACTCTCCACCGGAGAGT- GCTCTGTCAAGCGCGGGTCTCTCG 1132
Db      541  TCGGAGAGCACTACTCTCCACCGGAGAGT- GCTCTGTCAAGCGCGGGTCTCTCG 600
Oy      1133  GCGGAGGCGGAGGTTTACGCGCTTTCAGGCGCGCGAGAGAGAGAGAGAGAGAG 1192
Db      601  GCGGAGGCGGAGGTTTACGCGCTTTCAGGCGCGCGAGAGAGAGAGAGAGAGAG 660
Oy      1193  GCGGCGCGCGATTTCCCTGAGCTGTGGGAGTGCACCCAGAGACTGCGGCTCACAT 1252
Db      661  GCGGCGCGCGATTTCCCTGAGCTGTGGGAGTGCACCCAGAGACTGCGGCTCACAT 720
Oy      1253  CGCTTCTCTGTGTGGGAGGCGGAGTGGCGCATTCGCTACCGCTCCCGCGCACT 1312
Db      721  CGCTTCTCTGTGTGGGAGGCGGAGTGGCGCATTCGCTACCGCTCCCGCGCACT 780
Oy      1313  GGGGGCTTGTGAACCCCAAACTGACTGAGTGGCCAGTGTGCTCAAAATTGGCAGAG 1372
Db      781  GGGGGCTTGTGAACCCCAAACTGACTGAGTGGCCAGTGTGCTCAAAATTGGCAGAG 840
Oy      1373  ACGTGAAGGACACTCCAAAGTGGGCGCAAAATGAGTGGCAGTGGCGGGTGGCTGGA 1432
Db      841  ACGTGAAGGACACTCCAAAGTGGGCGCAAAATGAGTGGCAGTGGCGGGTGGCTGGA 900
Oy      1433  GCGGTCCTGCGTGTGCTCCGCTTTCGCTTGTGCTTAAAGTGTGATTAAC 1492
Db      901  GCGGTCCTGCGTGTGCTCCCGCTTTCGCTTGTGCTTAAAGTGTGATTAAC 960
Oy      1493  AACTTAGTCTGCTGTGCTGAG 1513
Db      961  AACTTAGTCTGCTGTGCTGAG 981

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RESULT 9
AAV63644

ID AAV63644 standard: DNA: 981 BP.

AAV63644:

15-FEB-1999 (first entry)

Human telomerase RNA component sequence from lambda clone 28-1.

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KW      Lambda clone 28-1; human; telomerase RNA component; anticancer therapy;
KM      assay; vaccine; cancer; purification; ss.
OS      Synthetic.
OS      Homo sapiens.
FH      Key
FT      Location/Qualifiers
FT      misc-feature
FT      266..716
FT      /tag= a
FT      /note= "human telomerase RNA component sequence"
PN      WO9845450-A1.
PD      15-OCT-1998.
PI      04-APR-1997; 97WO-US06012.
PF      04-APR-1997; 97WO-US06012.
PR      04-APR-1997; 97WO-US06012.
PX      (GERO-) GERON CORP.
PA      Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA,
PI      Vassero AP, Weinlich SL;
PX      WPI: 1998-594485/50.
XX      Purification of telomerase on affinity material - useful for, e.g.
XX      diagnosis and treatment of cancer
XX      Disclosure: Pages 14-15; 76pp: English.
XX      The present sequence represents the PstI fragment of the 2.4 kb
XX      Sautiral-HindIII fragment of lambda clone 28-1. This clone contains
XX      human telomerase RNA component gene sequences. The specification
XX      provides methods for purifying human telomerase. The methods involve
XX      the use of several sequential steps, including the use of two matrices
XX      that bind molecules bearing negative charges, a matrix that binds
XX      molecules bearing positive charges, an affinity purification step
XX      and a size separation. Telomerase is a particular target of anticancer
XX      therapies, and is useful in assays for characterizing (pre)cancerous
XX      cells. The present sequence can be used for such assays. Telomerase can
XX      also be used to screen for specific modulators, for biochemical analysis
XX      of its activity, and in preparation of antibodies. Fragments of
XX      telomerase, or nucleic acid encoding them, are used in vaccines, and
XX      for treating over expression of telomerase, particularly in cancer.
XX      Sequence 981 BP: 172 A; 303 C; 305 G; 200 T; 1 other;
SO

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Query Match 54.7%; Score 965.8; DB 19; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.6e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Oy      534  CTGCAAGAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGC 593
Db      1  CTGCAAGAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGC 60
Oy      594  TCGGAAGTAAGACGCAAAAGCCTTCCCGGAGCGTGGCGGAGGCAAGAGTCTCTCATG 653
Db      61  TCGGAAGTAAGACGCAAAAGCCTTCCCGGAGCGTGGCGGAGGCAAGAGTCTCTCATG 120
Oy      654  GCGGAAATGGAACCTTAAATTTCCCGTTCCCGCCAAACACCGCGCGGAGAGAGTACTC 713
Db      121  GCGGAAATGGAACCTTAAATTTCCCGTTCCCGCCAAACACCGCGCGGAGAGAGTACTC 180
Oy      714  TCACGAGAGCGCGAGAGTACAGTGGGCAATCCGTCGGTGGGCGCGCTCCCTTAT 773
Db      181  TCACGAGAGCGCGAGAGTACAGTGGGCAATCCGTCGGTGGGCGCGCTCCCTTAT 240
Oy      774  AAGCGGATCCCGCGCGACCGCGGTCGCGAGGGTGGGCTGGAGAGGGTGTGTC 833
Db      241  AAGCGGATCCCGCGCGACCGCGGTCGCGAGGGTGGGCTGGAGAGGGTGTGTC 300
Oy      834  CATTTTGTCTAACCTTAAGTGAAGAGGCGGTAGGCGCGCGTCTTGTGCTCCCGCGCG 893

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|||||
Db 301 CATTTTGTCTAACTAGAGAGGCGTAGGCGCTTGTGCTCCCGCGG 360
Oy 894 CTGTTTTCCTGCTGACTTTCAGCGGGGAAAAAGCCTGGCCTGCCCTTCCACCGTT 953
Db 361 CTGTTTTCCTGCTGACTTTCAGCGGGGAAAAAGCCTGGCCTGCCCTTCCACCGTT 420
Oy 954 CATTTAGAGCAAAATAATGTCACTGCTGGCCCTTCCCGGGAGACTGC 1013
Db 421 CATTTAGAGCAAAATAATGTCACTGCTGGCCCTTCCCGGGAGACTGC 480
Oy 1014 GCGGGTCCCTGCGCCAGCCCGGAAACCCCGCTGAGGCGCGGCTCCCGGGCTTC 1073
Db 481 GCGGGTCCCTGCGCCAGCCCGGAAACCCCGCTGAGGCGCGGCTCCCGGGCTTC 540
Oy 1074 TCCGGAGGACCTACTGACCGCCGGAAGATT-GGCTCTGTACGCCGGGCTCTCCGG 1132
Db 541 TCCGGAGGACCTACTGACCGCCGGAAGATTGCTGTACGCCGGGCTCTCCGG 600
Oy 1133 GCGGAGGCGGAGGTTTCAGGCTTTTCAGGCGCGAGAAAGAGAGAGGAGTCCCGCG 1192
Db 601 GCGGAGGCGGAGGTTTCAGGCTTTTCAGGCGCGAGAAAGAGAGAGGAGTCCCGCG 660
Oy 1193 CCGGCGCGATTCCTGAGACTGTGGAGCTGCACCCAGAGCTCGCTCAACATGAGATT 1252
Db 661 CCGGCGCGATTCCTGAGACTGTGGAGCTGCACCCAGAGCTCGCTCAACATGAGATT 720
Oy 1253 CGCTTTCCTGTGTGGGGGGAAGCGCGATCGTGGCGATCCGTCACCCCTCCCGGCAAT 1312
Db 721 CGCTTTCCTGTGTGGGGGGAAGCGCGATCGTGGCGATCCGTCACCCCTCCCGGCAAT 780
Oy 1313 GGGGCGTTGTGAACCCCAAACTGACTGACTGGGCGAGTGTCTCAAAATTGGAGAG 1372
Db 781 GGGGCGTTGTGAACCCCAAACTGACTGACTGGGCGAGTGTCTCAAAATTGGAGAG 840
Oy 1373 AGCTGAAGCACTCCAAAGTGGGCAAAATGAATGAGAGGCGGGGTTGCTTGA 1432
Db 841 AGCTGAAGCACTCCAAAGTGGGCAAAATGAATGAGAGGCGGGGTTGCTTGA 900
Oy 1433 GCGGTCCTGTGGGGGTTTCCCGCTTCCCGCTTGTGTGCTTGTATGTTATAC 1492
Db 901 GCGGTCCTGTGGGGGTTTCCCGCTTCCCGCTTGTGTGCTTGTATGTTATAC 960
Oy 1493 AACTTAGTTCCTGCTGCAG 1513
Db 961 AACTTAGTTCCTGCTGCAG 981

RESULT 10
AA23626
ID AA23626 standard: DNA; 981 BP.
XX
AC AA23626:
XX
DT 07-JAN-2000 (first entry)
XX
DE Human clone 28-1 containing telomerase fragment.
XX
KM Telomerase: human; immune response: cancer; vaccine: treatment;
KW disease: ss.
XX
OS Homo sapiens.
XX
PN US5968506-A.
PD 19-OCT-1999.
XX
PF 04-APR-1997; 97US-0833377.
XX
PR 04-AUG-1995; 95US-0510736.
XX
PA (GERO-) GERON CORP.
XX
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PI Atkinson EM, Lichtsteiner SP, Weinlich SL, Pruzan RA, Kealey JR;
PI Vasseroi AP;
XX
XX WPI: 1999-590379/50.
XX
XX Compositions comprising human telomerase, useful for treating diseases
XX associated with overexpression of telomerase e.g. cancer -
XX
XX Disclosure: Column 41-42: 34pp; English.
XX
XX This invention describes a novel composition comprising human telomerase
XX having at least 2000-fold (preferably at least 6000-fold) increased
XX relative purity compared with crude extract of cells from
XX adenovirus-transformed kidney cell line. The composition is useful for
XX eliciting an immune response in animals and may therefore be used as a
XX vaccine for treating diseases associated with the overexpression of
XX telomerase e.g. cancer. This sequence represents a nucleic acid fragment
XX from human clone 28-1 which contains a fragment of the human telomerase
XX described in the method of the invention.

SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.7%; Score 965.8; DB 20; Length 981;
Best Local Similarity 99.7%; Pred. No. 3,6e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 534 CTGCAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTACCTTTAAAGAG 593
Db 1 CTGCAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTACCTTTAAAGAG 60
Oy 594 TCGGAGTAAAGACGAAAGCCTTCCCGAGCTGGGAAAGGCAAGTCTCTCATG 653
Db 61 TCGGAGTAAAGACGAAAGCCTTCCCGAGCTGGGAAAGGCAAGTCTCTCATG 120
Oy 654 GCGGAAATGGAATTAAATTCCTGTCCTCCCAACAGCCCGCGGAGAGTACTC 713
Db 121 GCGGAAATGGAATTAAATTCCTGTCCTCCCAACAGCCCGCGGAGAGTACTC 180
Oy 714 TCACGAGACCGGAGAGTACGTTGCCAATCCGTCGCGGCGGCTTCTTAT 773
Db 181 TCACGAGACCGGAGAGTACGTTGCCAATCCGTCGCGGCGGCTTCTTAT 240
Oy 774 AAGCCGACTCGCCGCGACGCGACCGGTTGGCGAGAGTGGGCTGGAGGCTGTGCG 833
Db 241 AAGCCGACTCGCCGCGACGCGAGCGGTTCCGAGAGTGGGCTGGAGGCTGTGCG 300
Oy 834 CATTTTGTCTAACCTTAACAGAGGCGTAGGCGCGCTTGTCTCCCGCGCG 893
Db 301 CATTTTGTCTAACCTTAACAGAGGCGTAGGCGCGCTTGTCTCCCGCGCG 360
Oy 894 CTGTTTTCCTGCTGACTTTCAGCGGGGCGAAAAAGCCTGGCCTTGCCTTCACCGTT 953
Db 361 CTGTTTTCCTGCTGACTTTCAGCGGGGCGAAAAAGCCTGGCCTTGCCTTCACCGTT 420
Oy 954 CATTTAGAGCAAAATAATGTCACTGCTGGCCCTTCCCGGGAGACTGC 1013
Db 421 CATTTAGAGCAAAATAATGTCACTGCTGGCCCTTCCCGGGAGACTGC 480
Oy 1014 GCGGGTCCCTGCGCCAGCCCGGAAACCCCGCTGAGGCGCGGCTCCCGGGCTTC 1073
Db 481 GCGGGTCCCTGCGCCAGCCCGGAAACCCCGCTGAGGCGCGGCTCCCGGGCTTC 540
Oy 1074 TCCGGAGGACCTACTGACCGCCGGAAGATT-GGCTCTGTACGCCGGGCTCTCCGG 1132
Db 541 TCCGGAGGACCTACTGACCGCCGGAAGATTGCTGTACGCCGGGCTCTCCGG 600
Oy 1133 GCGGAGGCGGAGGTTTCAGGCTTTTCAGGCGCGAGAAAGAGAGGAGTCCCGCG 1192
Db 601 GCGGAGGCGGAGGTTTCAGGCTTTTCAGGCGCGAGAAAGAGAGGAGTCCCGCG 660
Oy 1193 CCGGCGCGATTCCTGAGACTGTGGAGCTGCACCCAGAGCTCGCTCAACATGAGATT 1252
Db 661 CCGGCGCGATTCCTGAGACTGTGGAGCTGCACCCAGAGCTCGCTCAACATGAGATT 720
```


QY 1253 CGCTTCCTGTTGGGGGGAACCCGATCGTGGCATCCGTCACCCCTGCGGAGT 1312
 |||||||
 Db 721 CGCTTCCTGTTGGGGGGAACCCGATCGTGGCATCCGTCACCCCTGCGGAGT 780
 QY 1313 GGGGCGTTGTAACCCCAACCTGACTAGTGGCCAGTGTGCGCAATTTGGAGAG 1372
 |||||||
 Db 781 GGGGCGTTGTAACCCCAACCTGACTAGTGGCCAGTGTGCGCAATTTGGAGAG 840
 QY 1373 AGGTGAAGGACCTCCAAAGTGGCCAAATGAATGGCAGTGAACCGGGTTGGCTGA 1432
 |||||||
 Db 841 AGGTGAAGGACCTCCAAAGTGGCCAAATGAATGGCAGTGAACCGGGTTGGCTGA 900
 QY 1433 GCGCTTCCGCTGGGTTCTCCGCTTCCGCTTTTGTGCTTTATGTTGTTATAC 1492
 |||||||
 Db 901 GCGCTTCCGCTGGGTTCTCCGCTTCCGCTTTTGTGCTTTATGTTGTTATAC 960
 QY 1493 AACTTAGTTCTGCTCTCCAG 1513
 |||||||
 Db 961 AACTTAGTTCTGCTCTCCAG 981

RESULT 11

AAA37564
 ID AAA37564 standard; DNA; 981 BP.

AC AAA37564;

XX 15-AUG-2000 (first entry)

XX Human telomerase nucleotide sequence.

DE Peptide nucleic acid; PNA: telomerase; ribonucleoprotein enzyme; cancer;
 KW Inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
 KW paternity testing; ds.

XX Homo sapiens.

OS US6046307-A.

XX 04-APR-2000.

XX 09-APR-1997; 97US-0838545.

XX 09-APR-1996; 96US-0630019.

PR (TEXA) UNIV TEXAS SYSTEM.

PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX WPI; 2000-292432/25.

PT New peptide nucleic acid (PNA) compounds that inhibit telomerase
 activity in mammalian cells is useful as probes to detect the RNA
 component of a mammalian telomerase

PS Disclosure: Column 13-14; 45pp; English.

CC The present sequence represents the human telomerase nucleotide sequence.
 CC to the mRNA component of mammalian telomerase, and inhibit telomerase
 CC activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one
 CC strand of the telomeric DNA, using as a template an 11 nucleotide
 CC sequence contained within the RNA component of the enzyme. The invention
 CC relates to PNA molecules having a sequence of no more than 25 bases,
 CC which include the sequence GTTAGG. The sequence of no more than 25 bases,
 CC backbone increases the melting temperature of associating strands,
 CC increases the rate of association with targeted nucleic acids, and
 CC affords greater resistance of degradation by proteases or nucleases. The
 CC therapeutic PNAs may be used for treating disease conditions such as
 CC cancer, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency

CC syndrome) and associated pathologies, fungal infections, and other
 CC diseases characterized by abnormal telomeric metabolism or telomerase
 CC activity. In combination with antineoplastic and other cytotoxic or
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
 CC used for molecular diagnostics, labelled PNAs are used as hybridization
 CC probes to detect or quantitate polynucleotides having a human telomerase
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification
 CC of individuals, e.g. paternity testing, based on hTR gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic
 CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component.

SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.7%; Score 965.8; DB 21; Length 981;
 Best Local Similarity 99.7%; Pred. No. 3.6e-261;
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 534 CTGCGAGAGATGAAAAAGGCGCTCTGATCACTCAAGTTAGTTTCACTTAAAGAG 593
 |||||||
 Db 1 CTGCGAGAGATGAAAAAGGCGCTCTGATCACTCAAGTTAGTTTCACTTAAAGAG 60
 QY 594 TCGGAAGTAAAGGCAAAAGCCTTCCCGGACGTGCGGAAGGCAAGTCCTCTCATG 653
 |||||||
 Db 61 TCGGAAGTAAAGGCAAAAGCCTTCCCGGACGTGCGGAAGGCAAGTCCTCTCATG 120
 QY 654 GCGGGAATGGAATTTATTTCCGTTCCCGCCACACAGCGCCGCGAGAGATGCTC 713
 |||||||
 Db 121 GCGGGAATGGAATTTATTTATTTCCCGTTCCCGCCACACAGCGCCGCGAGAGATGCTC 180
 QY 714 TCACGAGACCGCGGAGATCACTTGGCCAAATCCGTGCGGTGGCGGCGCCTCTTAT 773
 |||||||
 Db 181 TCACGAGACCGCGGAGATCACTTGGCCAAATCCGTGCGGTGGCGGCGCCTCTTAT 240
 QY 774 AAGCGACTGCGCGCGACGCGACCGGCGGAGGCGGCGGCGGAGAGGCGTGTGCG 833
 |||||||
 Db 241 AAGCGACTGCGCGCGACGCGACCGGCGGAGGCGGCGGAGAGGCGTGTGCG 300
 QY 834 CATTTTTCCTAAACCTTAAGTGAAGGCGTGAAGGCGGCTTTTGTCTCCCGCGG 893
 |||||||
 Db 301 CATTTTTCCTAAACCTTAAGTGAAGGCGTGAAGGCGGCTTTTGTCTCCCGCGG 360
 QY 894 CTGTTTTCCTGCTGACTTTCAGGCGGCGGAAAAAGCCTCGGCTGCGGCTTCACCGTT 953
 |||||||
 Db 361 CTGTTTTCCTGCTGACTTTCAGGCGGCGGAAAAAGCCTCGGCTGCGGCTTCACCGTT 420
 QY 954 CATTTCTAGACAAACAAAAATGTCAAGCTGCTGCGGCTTCGCGGAGACCTTCG 1013
 |||||||
 Db 421 CATTTCTAGACAAACAAAAATGTCAAGCTGCTGCGGCTTCGCGGAGACCTTCG 480
 QY 1014 GCGGCGTGCCTGCGCCAGCGCCCGAAGCCCGCTGGAAGGCGCGGCTGCGGCGGCTTC 1073
 |||||||
 Db 481 GCGGCGTGCCTGCGCCAGCGCCCGAAGCCCGCTGGAAGGCGCGGCTGCGGCGGCTTC 540
 QY 1074 TCGGAGAGCACTACTGCGCACCGCGAAGATT-GGCTGTGACGCGCGGCTTCGCGG 1132
 |||||||
 Db 541 TCGGAGAGCACTACTGCGCACCGCGAAGATTGGGTCTGTACGCGCGGCTTCGCGG 600
 QY 1133 GCGGAGGCGAGGTTGAGGCTTTTCAAGCGCCGAGAGAGAGAGAGAGAGAGTCCCGCG 1192
 |||||||
 Db 601 GCGGAGGCGAGGTTGAGGCTTTTCAAGCGCCGAGAGAGAGAGAGAGAGAGTCCCGCG 660
 QY 1193 GCGGCGCATTTCCCTGACCTGTGGAGCTGACACAGAGATCGGCTACACATTCATTT 1252
 |||||||
 Db 661 GCGGCGCATTTCCCTGACCTGTGGAGCTGACACAGAGATCGGCTACACATTCATTT 720
 QY 1253 CGCTTTCCTGTTGGGGGGAACCCGATCGTGGCATCCGTCACCCCTGCGGAGT 1312

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DB 721 CGCTTCTCTGTGGTGGGGGAACGCCGATCGTGGCATCCGTACACCCCTCGCGGAGT 780
      |||
QY 1313 GGGGGCTTGTGAACCCCAAACTGACTGCTGGCCAGTGTCTGCAATTGGCAGAG 1372
      |||
DB 781 GGGGGCTTGTGAACCCCAAACTGACTGCTGGCCAGTGTCTGCAATTGGCAGAG 840
      |||
QY 1373 ACGTGAAGCAGCTCCAAAGTCCGCAAAATGAATGGAGTGGCGGGGTTGCCGGA 1432
      |||
DB 841 ACGTGAAGCAGCTCCAAAGTCCGCAAAATGAATGGAGTGGCGGGGTTGCCGGA 900
      |||
QY 1433 GCGGTCCTGCGGAGTGTCTCCGCTTCGCTTTTGTGCTTTATGTTATTTAC 1492
      |||
DB 901 GCGGTCCTGCGGAGTGTCTCCGCTTCGCTTTTGTGCTTTATGTTATTTAC 960
      |||
QY 1493 AACTAGTCTGCTGCGAG 1513
      |||
DB 961 AACTAGTCTGCTGCGAG 981
      |||

RESULT 12
AAS15442
ID AAS15442 standard; DNA: 981 BP.
AC AAS15442;
XX
DT 14-FEB-2002 (first entry)
XX
DE Pelti fragment containing human telomerase RNA component gene sequence.
XX
KW Mammalian; forensic; paternity testing; human telomerase RNA component;
KW hmr gene RFLP pattern; cancer; inflammation; lymphoproliferative disease;
KW autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia;
KW HIV; AIDS; human immunodeficiency virus; telomere metabolism; cytosolic;
KW acquired immunodeficiency syndrome; anti-inflammatory; immunosuppressive;
KW bacteriophage lambda clone 28-1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 266..716
      /*tag= a
      /note= "htr gene sequence"
      /*tag= b
      /note= "template region of htr used as template for
      synthesis of telomeric repeats"
FT misc_feature 311..320
      /*tag= b
      /note= "template region of htr used as template for
      synthesis of telomeric repeats"
FT
XX
XX US6294650-B1.
XX
XX 25-SEP-2001.
XX
XX PD 08-JUL-1999: 99US-0349532.
XX
XX PF 09-APR-1997: 97US-0838545.
XX
XX PR 09-APR-1996: 96US-0630019.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Shay JW, Wright WE, Platyszek MA, Corey DR, Norton JC;
XX
XX WPI: 2001-638024/73.
XX
XX DR New peptide nucleic acids that hybridises to the RNA component of
XX PT mammalian telomerase, useful for treating or preventing cancer,
XX PT inflammation, lymphoproliferative diseases, autoimmune disease, or
XX PT neurodegenerative diseases -
XX
XX PS Disclosure: Column 13-16: 46pp; English.
XX
XX CC The present invention relates to peptide nucleic acids (PNAs), comprising
XX CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX CC mammalian cells by hybridising to the RNA component of mammalian
```

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CC telomerase. The PNAs are useful as probes to detect the RNA component
CC of mammalian telomerase and as inhibitors of telomerase activity, or to
CC detect and/or quantitate polynucleotide having the human telomerase
CC RNA component (htr) sequence, as well as in forensic identification of
CC individuals, such as paternity testing or identification of criminal
CC suspects or unknown descendants based on the htr gene RFLP pattern. The
CC PNA can be further used for treating or preventing cancer, inflammation,
CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC diseases. The PNAs in combination with other pharmaceuticals (such as
CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC diseases characterised by abnormal telomere metabolism or telomerase
CC activity. The present sequence represents a Pelti fragment, derived
CC from bacteriophage lambda clone 28-1, containing the htr gene sequence.
XX
SQ Sequence 981 BP: 172 A; 303 C; 305 G; 200 T; 1 other:
XX
Query Match 54.7%; Score 965.8; DB 23; Length 981;
Best Local Similarity 99.7%; Pred. No. 3, 6e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 534 CTCAGAGATAGAAAAAGCCCTGTGATACCTCAAGTAGTTTCACTTTAAAGAG 593
      |||
DB 1 CTCAGAGATAGAAAAAGCCCTGTGATACCTCAAGTAGTTTCACTTTAAAGAG 60
      |||
QY 594 TCGGAAGTAAAGACGCAACCTTTCCCGAGCTGGGGAAGGGCAGCTCTTCATG 653
      |||
DB 61 TCGGAAGTAAAGACGCAACCTTTCCCGAGCTGGGGAAGGGCAGCTCTTCATG 120
      |||
QY 654 GCGGAAATGGAACCTTAATTTCCCGTCCCAACACAGCCGCGGAGAGTGCATC 713
      |||
DB 121 GCGGAAATGGAACCTTAATTTCCCGTCCCAACACAGCCGCGGAGAGTGCATC 180
      |||
QY 714 TCACGAGAGCCGGAGAGTACGCTTGCCCAATCCGTGCGTGGCGGCTCCCTTAT 773
      |||
DB 181 TCACGAGAGCCGGAGAGTACGCTTGCCCAATCCGTGCGTGGCGGCTCCCTTAT 240
      |||
QY 774 AAGCCGACGCGCCGAGCGACCGGCTTGCGAGGCTGGGAGGGGTGGG 893
      |||
DB 241 AAGCCGACGCGCCGAGCGACCGGCTTGCGAGGCTGGGAGGGGTGGG 300
      |||
QY 834 CATTCTTGTCTAACCTTAATGAGAGGCGTGAAGCGCGCTTTTGTCCCGCGC 893
      |||
DB 301 CATTCTTGTCTAACCTTAATGAGAGGCGTGAAGCGCGCTTTTGTCCCGCGC 360
      |||
QY 894 CTGTTTCTGCGTACTTTCACGCGGGGAAAAAGCCTGCGGCTTCCACCGTT 953
      |||
DB 361 CTGTTTCTGCGTACTTTCACGCGGGGAAAAAGCCTGCGGCTTCCACCGTT 420
      |||
QY 954 CATTCTAGACCAAAATATGTCAAGTGTGGCCGCTTCCCGGGGAGCTGC 1013
      |||
DB 421 CATTCTAGACCAAAATATGTCAAGTGTGGCCGCTTCCCGGGGAGCTGC 480
      |||
QY 1014 GCGGAGTCCGCTGCCAGCCCGCAACCCGCTGAGAGCGGCGGTGGCGGGGCTTC 1073
      |||
DB 481 GCGGAGTCCGCTGCCAGCCCGCAACCCGCTGAGAGCGGCGGTGGCGGGGCTTC 540
      |||
QY 1074 TCCGAGGACACTACTGCAACCGGAAAGATT--GGCTGTGTACCGCGGCTTCTCGGG 1132
      |||
DB 541 TCCGAGGACACTACTGCAACCGGAAAGATTGGGCTGTGTACCGCGGCTTCTCGGG 600
      |||
QY 1133 GCGGAGGCGAGGTTCAGGCTTTCAGGCGGCAAGAGAGAGGAGGAGTCCCGCG 1192
      |||
DB 601 GCGGAGGCGAGGTTCAGGCTTTCAGGCGGCAAGAGAGAGGAGGAGTCCCGCG 660
      |||
QY 1193 GCGGAGGCGAGTTCCTGAGTGTGGAGCTGACCCAGAGCTGCGGCTCAACATGCAATT 1252
      |||
DB 661 GCGGAGGCGAGTTCCTGAGTGTGGAGCTGACCCAGAGCTGCGGCTCAACATGCAATT 720
      |||
QY 1253 CGCTTCTCTGTGGTGGGGGAACGCCGATCGTGGCATCCGTACACCCCTCGCGGAGT 1312
      |||
DB 721 CGCTTCTCTGTGGTGGGGGAACGCCGATCGTGGCATCCGTACACCCCTCGCGGAGT 780
      |||
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QY 1313 GGGGGCTTGTGAACCCCAACCTGACTGCTGCCAGTGTGTCGCAAAATTTGGCAGAG 1372
 |||||||
 Db 781 GGGGGCTTGTGAACCCCAACCTGACTGCTGCCAGTGTGTCGCAAAATTTGGCAGAG 840
 QY 1373 ACCTGAAGGACCTCCAAAGTGGCCAAATGAATGGCAGTGGCCGGGTTGGCTGGA 1432
 |||||||
 Db 841 ACCTGAAGGACCTCCAAAGTGGCCAAATGAATGGCAGTGGCCGGGTTGGCTGGA 900
 QY 1433 GCGGTCCTGGCGGGTGTCTCCGCTTTCCTTTTGTTCCTTTTATGTTATTTAC 1492
 |||||||
 Db 901 GCGGTCCTGGCGGGTGTCTCCGCTTTCCTTTTGTTCCTTTTATGTTATTTAC 960
 QY 1493 AACTAGTTCCTGCTTCGAC 1513
 |||||||
 Db 961 AACTAGTTCCTGCTTCGAC 981

RESULT 13
 AAS09471
 ID AAS09471 standard; DNA; 980 BP.
 XX

AC AAS09471;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human DNA containing the RNA component of telomerase.
 XX
 KW Human; Telomerase; RNA component; vaccine; antibody; cancer; EF2H;
 KW nucleolin; ds.
 XX
 OS Homo sapiens.
 XX
 FH
 FT misc-feature
 FT 21
 FT Location/Qualifiers
 FT /tag= a
 FT /note= "Designated 0 in the specification, with 7
 FT in the complementary strand"
 FT 311..320
 FT /tag= b
 FT /label= "template_region"
 FT /note= "This region is not further defined in the
 FT specification"

XX US6261556-B1.
 XX
 PN 17-JUL-2001.
 PD
 XX
 PE 18-OCT-1999; 99US-0420056.
 XX
 PR 04-APR-1997; 97US-0833377.
 PR 04-AUG-1995; 95US-0510736.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA,
 PI Kealey JT;
 DR WPI: 2001-450477/48.
 XX
 PT Purified human telomerase, useful for inducing immune response in
 PT animals, comprises several thousand folds increased purity compared
 PT with cytoplasmic crude cell preparations -
 XX
 PS Disclosure: Column 9-12; 29pp; English.

CC The sequence contains human telomerase, hTR, RNA component. The invention
 CC relates to a purified human telomerase core enzyme protein comprising
 CC 2000-fold increased purity compared with a crude extract of cells from
 CC adenovirus-transformed kidney cell line (293 cells) and when associated
 CC with telomerase RNA component has DNA polymerase activity and a molecular
 CC weight of 200-2000 kilo daltons (kda) The purified telomerase is useful
 CC for inducing a humoral or cell-mediated immune response in an animal.

CC Purified telomerase or immunogenic fragments are useful as vaccines for
 CC treating diseases associated with over-expression of telomerase, such as
 CC cancer and for producing antibodies that recognize telomerase, which are
 CC useful as affinity agents in isolating the proteins and for detecting the
 CC presence of proteins in a sample, such as cell or tissue. Identification
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
 CC Telomerase and/or telomerase associated proteins are also useful for
 CC screening compounds to identify agents that alter the association of
 CC telomerase-associated proteins, such as nucleolin or EF2H with
 CC telomerase.

Sequence 980 BP: 171 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.1%; Score 954.4; DB 22; Length 980;
 Best Local Similarity 99.6%; Pred. No. 5.9e-258;
 Matches 977; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 534 CTGCAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAAAG 593
 |||||||
 Db 1 CTGCAGAGATAGAAAAAGNCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAAAG 60
 QY 594 TCGGAAGTAAGAGCAAGCCCTTCCCGAGCTGGCGAAGGCAACGCTTCTCATG 653
 |||||||
 Db 61 TCGGAAGTAAGAGCAAGCCCTTCCCGAGCTGGCGAAGGCAACGCTTCTCATG 120
 QY 654 GCGGGAATGGAATTAAATTTCCGTTCCCCCAACAGCCCGCGAGAGTGAATC 713
 |||||||
 Db 121 GCGGGAATGGAATTAAATTTCCGTTCCCCCAACAGCCCGCGAGAGTGAATC 180
 QY 714 TCACGAGACCGCGAGAGTCACTTGGCAATCCGTGCGGTGGGCGGCTCCCTTAT 773
 |||||||
 Db 181 TCACGAGACCGCGAGAGTCACTTGGCAATCCGTGCGGTGGGCGGCTCCCTTAT 240
 QY 774 AAGCCGACTGCGCCGCGACGCGGCTTGGCGAGGCGGCGTGGAGGGGTGTGTC 833
 |||||||
 Db 241 AAGCCGACTGCGCCGCGACGCGGCTTGGCGAGGCGGCGTGGAGGGGTGTGTC 300
 QY 834 CATTTTCTCAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAAC 893
 |||||||
 Db 301 CATTTTCTCAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAAC 360
 QY 894 CTGTTTCTCGCTGACTTTCAGCGGGGGAAGCCCTGCGGCGGCTTTCACCTT 953
 |||||||
 Db 361 CTGTTTCTCGCTGACTTTCAGCGGGGGAAGCCCTGCGGCGGCTTTCACCTT 420
 QY 954 CATTTAGAGCAAAACAAATATGCTGCTGCGGCTTCCGCTTCCGCGGAGCTTGC 1013
 |||||||
 Db 421 CATTTAGAGCAAAACAAATATGCTGCTGCGGCTTCCGCTTCCGCGGAGCTTGC 479
 QY 1014 GCGGCTGCGCTGCGCAACCCCGCAACCCCGCTGAGAGCGCGGCTGCGGCGGCTTGC 1073
 |||||||
 Db 480 GCGGCTGCGCTGCGCAACCCCGCAACCCCGCTGAGAGCGCGGCTGCGGCGGCTTGC 539
 QY 1074 TCCGAGAGCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1132
 |||||||
 Db 540 TCCGAGAGCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
 QY 1133 GCGAGGCGAGGCTTCAAGCGCTTCAAGCGGCGAGAGAGAGAGAGAGAGAGAGAG 1192
 |||||||
 Db 600 GCGAGGCGAGGCTTCAAGCGCTTCAAGCGGCGAGAGAGAGAGAGAGAGAGAGAGAG 659
 QY 1193 GCGGCGGATTCCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1252
 |||||||
 Db 660 GCGGCGGATTCCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 719
 QY 1253 CGCTTTCCTGTTGGTGGGGGAAGCCGATGCTGCGATCCGTCACCCCTCGCGCACT 1312
 |||||||
 Db 720 CGCTTTCCTGTTGGTGGGGGAAGCCGATGCTGCGATCCGTCACCCCTCGCGCACT 779
 QY 1313 GGGGGCTTGTGAACCCCAACCTGACTGACTGAGGCGCAATGTGCAATTTGGCAGAG 1372
 |||||||
 Db 780 GGGGGCTTGTGAACCCCAACCTGACTGACTGAGGCGCAATGTGCAATTTGGCAGAG 839

QY	1373	ACGGAAGGACACCTCCAAAGCTCGCCAAAATGAATGGAGAGAGACCGGGGTTGGCTGGA	1433		
Db	840	ACGTGAAGGACACCTCCAAAGCTCGCCAAAATGAATGGAGAGAGACCGGGGTTGGCTGGA	899		
QY	1433	GCCGTCCTCGTGGGATTCCTCCGCTTCGCGCTTTTGTTCGCTTTATGATGTTATTTAC	1492		
Db	900	GCCGTCCTCGTGGGATTCCTCCGCTTCGCGCTTTTGTTCGCTTTATGATGTTATTTAC	959		
QY	1493	AACTTACTTCCTGCTGTCGAG	1513		
Db	960	AACTTACTTCCTGCTGTCGAG	980		
RESULT 14					
AAAT69188					
ID	AAAT69188	standard; DNA; 4118 BP.			
XX	AAAT69188;				
DT	26-FEB-1998	(first entry)			
DE	Construct pGEM-hTR containing RNA component of human telomerase.				
XX					
KW	Human telomerase: quantification; tumour cell; pGEM-hTR;				
KW	telodectinoma; melanoma; carcinoma; cancer; tumour; neuroblastoma;				
KW	rhabdomyosarcoma; leiomyosarcoma; lymphoma; RNA component; ss.				
OS	Homo sapiens.				
XX	Synthetic.				
FT	Key	Location/Qualifiers			
FT	misc_feature	12..975			
FT	FT	/*tag= a			
XX	/note= "CDNA from RNA component of human telomerase"				
PN	MO9718322-A2.				
PD	22-MAY-1997.				
XX					
XX	14-NOV-1996;	96MO-DE02183.			
XX					
PR	16-NOV-1995;	95DE-4042795.			
XX					
PA	(DAHM/) DAHM M W.				
PI	DAHm MW;				
DR	WPI: 1997-289298/26.				
XX					
PT	Quantifying tumour cells in body fluid - by measuring RNA component				
PT	of telomerase after amplification, especially useful for early				
PT	diagnosis of metastasis				
XX					
PS	Example 5; Fig 5; 46pp; German.				
XX					
CC	The present sequence is the construct pGEM-hTR, which comprises the				
CC	transcription vector pGEM-132ff(+) and the cDNA from the RNA				
CC	component of human telomerase. The construct was used in the				
CC	development of a novel method for quantifying tumour cells in a				
CC	body fluid. The method comprises specific amplification of the RNA				
CC	component of telomerase, and measuring the amount of amplified				
CC	nucleic acid. At least 1, preferably all 3 (AAAT69173-75) standard				
CC	nucleic acids are present (at different concentrations) and are				
CC	co-amplified with telomerase DNA. The amplification products are				
CC	detected directly or via a label or by hybridisation with a				
CC	labelled oligonucleotide (AAAT69184-87, 1 for each standard and 1 for				
CC	telomerase) and the amount of telomerase product compared with				
CC	that from the standards.				
CC	The method can be used to detect tumour cells, specifically				
CC	micrometastases, in a body fluid, particularly for the early				
CC	diagnosis of metastatic spread and for monitoring tumour therapy.				
CC	Typical tumour cells that can be quantified are micrometastases.				

CC	T cell lymphoblastoma or leukaemia (chronic myelogenous, and
CC	chronic or acute lymphatic leukaemia), teratocarcinoma, melanoma,
CC	carcinoma of lung, liver or prostate, cancer of colon or breast,
CC	kidney, brain or adrenal tumours, neuroblastoma, rhabdomyosarcoma,
CC	leiomyosarcoma and/or lymphoma.
xx	
50	Sequence 4118 BP; 991 A; 1032 C; 1094 G; 1001 T; 0 other:
	Query Match 50.1%; Score 883.4; DB 18; Length 4118;
	Best Local Similarity 97.6%; Pred. No. 1.2e-237;
	Matches 950; Conservative 0; Mismatches 16; Indels 7; Gaps
QY	794 GCACCGGGTTCGGAGAGGTGGGCTGGAGAGGTTGGTGGCCATTTTGTCTCAACCCCTAA 853
DB	14 GCCCGGGTTCGGAGAGGTGGGCTGGAGAGGTTGGTGGCCATTTTGTCTCAACCCCTAA 73
QY	854 CTGAGAGAGGCGTAGAGGCGCGTCTTTTCTCCCGCGCGGTGTTTCTCGCTACTTT 913
DB	74 CTGAGAGAGGCGTAGAGGCGCGTCTTTTCTCCCGCGCGGTGTTTCTCGCTACTTT 133
QY	914 CAGCGGGGGAAGAGCCCTCGGCTGGCGGCTTGCACCGTTCAFTCTAGACAAACAAAA 973
DB	134 CAGCGGGGGAAGAGCCCTCGGCTGGCGGCTTGCACCGTTCAFTCTAGACAAACAAAA 193
QY	974 ATGTCACTGTGTGGCCGCTTGCCCTCCCGGGAGACTCGCGCGGGTGCCTGCCAACC 1033
DB	194 ATGTCACTGTGTGGCCGCTTGCGCTGCGCTGCGCGGGAGCTTCGCGCGGGTGCCTGCCAACC 251
QY	1034 CCCGACACCCGCGGAGGCGCGGCGGTGGCGCGGGGCTTCTCGGAGGAGCACTACTGCA 1093
DB	252 CCCGACACCCGCGCTGGA -GCCGCGGTGGCGCGGGGCTTCTCGGAGGACCCACTGCA 310
QY	1094 CCGGAGAGATT -GGCTGTGCAACCGCGGGGTCTCTGGGGGCGAGGGGAGTTCAAGC 1152
DB	311 CCGGAGAGATTGGGCTGTGCAACCGCGGGGTCTCTGGGGGCGAGGGGAGGTTCA -CC 369
QY	1153 CTTTCAGCGCGCGAGAGAGGAACGAGAGATCCCCGCGCGCGCGGATCTCCTGAGC 1212
DB	370 GTTTCAGCGCGCGAGAGAGGAACGAGAGATCCC -GCCGCGCGCGGATCTCCTGAGC 427
QY	1213 TGTGGGACGTGACCCGAGACCTGGGCTGCACACTGTGAGTTGCTTCCGTGGTGGGGG 1272
DB	428 TGTGGGACGTGACCCGAGACCTGGGCTGCACACTGTGAGTTGCTTCCGTGGTGGGGG 487
QY	1273 GAACCGCGATCTGCGCATCCGTACACCCCTCGCGCGGCACTGGGGGCTTGTGAACCCCAA 1332
DB	488 GAACCGCGATCTGCGCATCCGTACACCCCTCGCGCGGCACTGGGGGCTTGTGAACCCCAA 547
QY	1333 ACCTGACTGACTGGGCCAGTGTGCTCTCAATTGGCAGAGACTGAAGCACTCCAAG 1392
DB	548 ACCTGACTGACTGGGCCAGTGTGCTCTCAAAATTGGCAGAGAGTGAAGCACTCCAAG 607
QY	1393 TCGGGCAAAATGAATGGGCAGTAGCGCGGGTTCCTGAGACCGTTCCTGCTGGGTCT 1452
DB	608 TCGGGCAAAATGAATGGGCAGTAGCGCGGGTTCCTGAGACCGTTCCTGCTGGGTCT 667
QY	1453 CCGGCTCTCCGCTTTTGTGACCTTTTATGGTGTATTAACAATTAGTTCCGTCTGCA 1512
DB	668 CCGGCTCTCCGCTTTTGTGACCTTTTATGGTGTATTAACAATTAGTTCCGTCTGCA 727
QY	1513 GATTTGTGAGGTTTGTGCTTCTCCCAAGAGATCTGACACAGTCCCTCAACGGGGT 1572
DB	728 GATTTGTGAGGTTTGTGCTTCTCCCAAGAGATCTGACACAGTCCCTCAACGGGGT 787
QY	1573 GTGGGAGAACAGTCATTTTGTGAGAGATCTATTAACATTTAATGATATTATTAAG 1632
DB	788 GTGGGAGAACAGTCATTTTGTGAGAGATCTATTAACATTTAATGATATTATTAAG 847
QY	1633 AAGATCTAAATGAACATTTGGAATTTGTGCTTAATGCTATCGGTTTATGCCAGAG 1692
DB	848 AAGATCTAAATGAACATTTGGAATTTGTGCTTAATGCTATCGGTTTATGCCAGAG 907
QY	1693 TTAGACATTTCTTTTGAATAATAGACTTGGGATGACCTTGAGCAGTAGATATATA 1752

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Db 908 TTAGAGTTCTTTTGAATAAGACCTTGGGATGACCTTACAGTATGATATA 967
Oy 1753 CCCCCAACAGCTT 1765
Db 968 CCCCCAACAGCTT 980

RESULT 15
AAT85371
ID AAT85371 standard: DNA; 962 BP.
XX
AC AAT85371:
XX
DT 15-APR-1998 (first entry)
XX
DE Human telomerase RNA component gene.
XX
KW Telomerase gene; transgenic organism; carcinogen; neoplastic growth;
XX cell growth; cell senescence; human; ss.
XX
OS Homo sapiens.
XX
PN MO9735967-A2.
XX
PD 02-OCT-1997.
XX
PF 21-MAR-1997; 97MO-US05070.
XX
PR 28-MAR-1996; 96US-0623166.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
PI DePinho RA, Greider C, Lee H, Marhunda MAB;
XX
XX WPI; 1997-489631/45.
XX
DR Non-human transgenic animal not expressing endogenous telomerase -
PT useful to test the carcinogenicity of a test compound, or to study
PT cell growth, division or senescence
XX
PS Disclosure: Fig 5: 58pp; English.
XX
XX
CC This sequence represents the human telomerase RNA component gene. This
CC sequence can be used in the transgenic organism of the invention. The
CC organism is a non-human transgenic organism in which at least one
CC endogenous telomerase gene encoding a telomerase component is altered and
CC telomerase activity is altered or is not expressed. The transgenic
CC organisms can be used as models to study telomerase activity. They can
CC also be used as a system to test compounds suspected of being
CC carcinogenic by exposing animals to the compound and determining
CC neoplastic growth as an indicator of carcinogenicity. The cells and
CC derived tissues are used to study cell growth and division and cell
CC senescence. The organisms are able to produce cells and tissues that, in
CC their wild type form, cannot be easily studied in vitro due to undergoing
CC small numbers of cell divisions.
XX
SQ Sequence 962 BP; 178 A; 257 C; 288 G; 239 T; 0 other;

Query Match 49.8%; Score 881.6; DB 18; Length 962;
Best local similarity 97.8%; Pred. No. 1.8e-237;
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Job time : 312 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 : Search time 3240 Seconds
(without alignments)
15853.843 Million cell updates/sec

Title: US-09-601-267-1

Perfect score: 1765

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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6	1719.6	97.4	2426	6	AR075507 Sequence
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8	1719.6	97.4	2426	6	AR161905 Sequence
9	1661.2	94.1	2420	6	I31750 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO9938964.

ACCESSION AX019547

VERSION AX019547.1 GI:10043461

KEYWORDS human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1765)

AUTHORS Keith,W.N.

TITLE Promoter regions of the mouse and human telomerase rna component genes

Pred. No. is the number of results predicted by chance to have a

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 VERSION AF047386.1 GI:300555
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REFERENCE 1 (bases 1 to 1765)
AUTHORS Zhao, J. Q., Hoare, S. F., McFarlane, R., Muir, S., Parkinson, E. K.,
Black, D. M., and Keith, W. N.
TITLE Cloning and characterization of human and mouse telomerase RNA gene
JOURNAL Promoter sequences
MEDLINE Oncogene 16 (10), 1345-1350 (1998)
PUBMED 98206512
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REFERENCE 2 (bases 1 to 1765)
AUTHORS Zhao, J. Q., Hoare, S. F., McFarlane, R., Muir, S., Parkinson, E. K.,
Black, D. M., and Keith, W. N.
TITLE Direct Submission
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REFERENCE 1 (bases 1 to 145829)
AUTHORS Mizuy,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Aisbrook,S.L., Amaralung,H.C., Are,J.R., Ayele,M., Banks,T.,
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Tansey,J., Taylor,C., Taylor,T., Tellford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watling,S.,
Williams,G., Williamson,A., Wlarczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 145829)
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
SUBMITTED (04-AUG-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 145829)
Worley,K.C.
Direct Submission

JOURNAL
Submitted (19-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 13, 2002 this sequence version replaced gi:20514648.
COMMENT
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HRTL
Center clone name: RP11-816J6
----- Summary Statistics
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye 65% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 145499 bases at least Q40
Consensus quality: 145597 bases at least Q30
Estimated insert size: 148612; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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VERSION AR016035.1 GI:3972312
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  Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
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JOURNAL
Patent: US 5958680-A 4 28-SEP-1999;
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Location/Qualifiers
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BASE COUNT 620 a 575 c 650 g 581 t
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 Db 1921 CTGTTGTGTGGGGAAGCGCGATCTGTGCGCATCTGCGCGCTGCGCGCACTGGGCGT 1980
 Qy 1320 TGTGAAACCCCAAACTGACTGTGGGCGCACTGTGCGCAATTTGGCAGGAGAGCTGAA 1379
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 Db 2041 GGCACCTCCAAAGTGGCCAAATGAGTGGCAGTGGCGGCGGCTGTGCGAGCGCTTC 2100
 Qy 1440 CTGCGTGGGTTCTCCGCTTCTGCTTTTGTGCTTTTATGTTTATTAACAATTAG 1499
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Qy 1500 TTCTGCTCTGACAGATTTTGTGAGGTTTGTGCTTCGCCAAGTAGATGTGACGAGTC 1559
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 Db 2341 TTTATGCGAGAGTTTGAAGTTTCTTTTGAATAAATTAAGACTTGGCGATGACCTTGAG 2400
 Qy 1740 CAGTAGATTAATACCCCAAGCTT 1765
 Db 2401 CAGTAGATTAATACCCCAAGCTT 2426

RESULT 7
 AR081664
 LOCUS AR081664 2426 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 1 from patent US 5972605.
 ACCESSION AR081664
 VERSION AR081664.1 GI:10008390
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2426)
 AUTHORS Villepontoux,B. and Harley,C.
 TITILE Assays for regulators of mammalian telomerase expression
 JOURNAL Patent: US 5972605,A1 26-OCT-1999
 FEATURES
 source 1..2426
 BASE COUNT 620 a 575 c 650 g 581 t
 ORIGIN

Query Match 97.4%; Score 1719.6; DB 6; Length 2426;
 Best Local Similarity 99.1%; Pred. No. 0; Mismatches 14; Indels 2; Gaps 2;
 Matches 1750; Conservative 0;

Qy 1 ACCTACTAGAGGCTGAGACACGAAATGCTGAAACCCGAGGAGCAGAGTTGCAGTG 60
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 Qy 181 CAGCACTCTTTAAGCAAACTCAATGTTGAAACGCCCTTTCTTCTAATTAAGGAG 240
 Db 841 CAGCACTCTTTAAGCAAACTCAATGTTGAAACGCCCTTTCTTCTAATTAAGGAG 900
 Qy 241 ATTCACTCTTAAGATTAAATATGTAGTACTTACCTTGAATTAAGCAATCTGTGTC 300
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 Qy 301 AGGAGAGCTGGAGAGGCAATTTCTAAGAAAAAGGGCAGGTTGGAATCTGGAGCATC 360
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 Qy 361 CCACTGAGCGGAGACAGATTGCTGCTTACTCACTGTGCTGCTGGAACTATTTTACAA 420
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Oy 421 AGTCTCCAAAAATGTGATGATCAAAACTAGAAATTAGTGTCTGTCTTAGGCCCTA 480
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Oy 1320 TGTGAACCCCAAACTGACTGATGAGGCGAGTGTGCTCAAAATTTGGAGAGAGCTGAA 1379
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Db 2401 CAGTAGATATAACCCCAAGCTT 2426

RESULT 8
AR161905
LOCUS AR161905 2426 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 3 from patent US 6258535.
ACCESSION AR161905
VERSION AR161905.1 GI:16228915
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeponteau, B., Feng, J., Funk, W. and Andrews, W. H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 3 10-JUL-2001;
FEATURES
source 1..2426
BASE COUNT 620 a 575 c 650 g 581 t
ORIGIN

Query Match 97.4%; Score 1719.6; DB 6; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;
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QY	601	TAAAGACGCAAAAGCTTTTCCCGAGAGTGTGGGAAGGCAAGTCTTCTCATGTGCGGAA	660
Db	1261	TAAAGACGCAAAAGCTTTTCCCGAGAGTGTGGGAAGGCAAGTCTTCTCATGTGCGGAA	1320
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QY	721	AGCCCGAGAGTCAAGCTTTGGCCAAATCCGTGCGGTGGCGGCGCTCTCTTTAAAGCCGA	780
Db	1381	AGCCCGAGAGTCAAGCTTTGGCCAAATCCGTGCGGTGGCGGCGCTCTCTTTAAAGCCGA	1440
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Db	1441	CTCGCCCGGACGCGCACCGGCTTCCGAGGCTGTGGAGGGGTGGTGGCCATTTT	1500
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Db	1681	CGCCGTGCCAGCCCCCGCAACCCGCTGTGAAGCGCGCGTGTGCGCCGCGGCTTCTCCGAG	1740
QY	1081	GCACCTACTGTGCACCGGAGAGATTT-GGCTGTGTACGCGCGCGGTCTCTCGGGGCGAG	1139
Db	1741	GCACCTACTGTGCACCGGAGAGATTTGGCTGTGTACGCGCGCGGTCTCTCGGGGCGAG	1800
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D _b	2281	AATATTAAATTAGAAGATCTTAATAAGAACTTGAATAATGTCTTTAATGTCATCGG	2340
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D _b	2401	CAGTAGATATTAACCCCACACAGCTT	2426

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 DEFINITION Sequence 3 from patent US 5583016
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 ACCESSION
 VERSION 131750.1 GI:1822541
 KEYWORDS
 SOURCE
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 2420)
 AUTHORS Villeneuve-Berg, J., Funk, W. and Andrews, W.H.
 TITLE Mammalian telomerase
 JOURNAL Patent-US-5583016 A 3 10-DEC-1996;
 FEATURES
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 1. 2420
 Location/Qualifiers
 /organism="unknown"
 BASE COUNT 620 a 572 c 647 g 581 t
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Db	721	AGCGAGATCAAGCCACATAGACTCATCCAGCTGGGGGAAAGACCAAGACTCCGTGCA	780
QY	121	AAAAAAAAATCGTTACAAATTTAGTGGATTTACTCCCTCTTTTACCATCAAGACA	180
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QY	181	CAGACTACTTTAAAGCAAACTCAATGATTTAAAGCGCTTCTTCTTAAATPAAAGGAG	240
Db	841	CAGACTACTTTAAAGCAAACTCAATGATTTAAAGCGCTTCTTCTTAAATPAAAGGAG	900
QY	241	ATTGAGTCCTTAAGATTATATATGAGTAGTTACACTGGATTAAAGCCATCCCTGCGCA	300
Db	901	ATTGAGTCCTTAAGATTATATATGAGTAGTTACACTGGATTAAAGCCATCCCTGCGCA	960
QY	301	AGGAAAGCTTGAGAGAAGGCATTTCTAAGGAAAAAAGGGGAGGGTTGGAACTCGGAGCATC	360
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QY	361	CCACTGAGCCGAGACAGATTTCGCTGAGTCATGCTGCTGGGAATCTATTTTCACAA	420
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Db 2395 CAGTAGATATAACCCCAAGCTT 2420

RESULT 10
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LOCUS AR081665 981 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 2 from patent US 5972605.
ACCESSION AR081665
VERSION AR081665.1 GI:10008391
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 981)
AUTHORS Villepontoux B. and Harley C.
TITLE Assays for regulators of mammalian telomerase expression
JOURNAL Patent: US 5972605-A 2 26-OCT-1999;
FEATURES
source
1..981
location/Qualifiers
BASE COUNT 172 a 303 c 306 g 200 t
ORIGIN

Query Match 54.8%; Score 967.4; DB 6; Length 981;
Best Local Similarity 99.8%; Pred. No. 4,7e-224;
Matches 979; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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DEFINITION Sequence 5 from patent US 5858777.
VERSION AR028774
ACCESSION AR028774.1 GI:5940747
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 981)
AUTHORS Villeporteu,B., Feng,J., Andrews,W.H. and Adams,R.R.
TITLES Methods and reagents for regulating telomere length and telomerase
activity
JOURNAL Patent: US 5858777-A 5 12-JAN-1999;
FEATURES
Location/Qualifiers
source 1..981
BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

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Query Match 54.8%; Score 966.4; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 8.2e-224;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 961 AACTTAGTTCCTGCTCTGACG 981

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DEFINITION Sequence 5 from Patent EP0953042.
VERSION AX022166
ACCESSION AX022166
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 981)
AUTHORS Andrews,W.H., Villeporteu,B., Adams,R.R. and Feng,J.
TITLES Methods and reagents for regulating telomere length and telomerase

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 GERON CORP (US)
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 misc_RNA
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 /note="HTR TRANSCRIPT SERVES AS TEMPLATE IN THE TELOMERASE
 RIBONUCLEOPROTEIN"

BASE COUNT 172 a 303 c 305 g 200 t 1 others
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Query Match 54.8%; Score 966.4; DB 6; Length 981;
 Best Local Similarity 99.7%; Pred. No. 8.2e-224;
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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 DEFINITION Sequence 1 from Patent W09845450.
 ACCESSION A84591
 VERSION A84591.1 GI:6733507
 KEYWORDS

SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 981)
 AUTHORS Atkinson,E.M. and Kealey,J.T.
 TITLE PURIFIED TELOMERASE
 JOURNAL Patent: WO 9845450-A 1 15-OCT-1998;
 GERON CORP (US)

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 266..716
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 /note="RNA COMPONENT OF HUMAN TELOMERASE (HTR)"

BASE COUNT 172 a 303 c 305 g 200 t 1 others
 ORIGIN

Query Match 54.7%; Score 965.8; DB 6; Length 981;
 Best Local Similarity 99.7%; Pred. No. 1.1e-223;
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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 DB 61 TCGGAAGTAAGACGCAAAACCTTTCCCGAGCTGCGGAAGGCGCAACGTCCTTCATG 120
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VERSION	AR079888.1	GI:10006641		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 981)			
TITLE	Weinrich, S.L., Atkinson, E.M. III, Lichtsteiner, S.P., Vassero, A.P., Pruban, R.A. and Keasley, J.T.			
	Purified telomerase			

JOURNAL Patent: US 5968506-A 1 19-OCT-1999;
 FEATURES Location/Qualifiers
 source 1. 981
 BASE COUNT 172 a 303 c 305 g 200 t 1 others
 ORIGIN

Query Match 54.7%: Score 965.8; DB 6; Length 981;
 Best local similarity 99.7%; Pred. No. 1.1e-223;
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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 Db 181 TCACGAGAGCCGAGAGTACGCTTGCCCAATCCGTCGCGCGCGCTTCCTTAT 240
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SUMMARIES

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3	1719.6	97.4	2426	2 US-08-472-802C-4	Sequence 4, Appl1
4	1719.6	97.4	2426	2 US-08-714-482-1	Sequence 1, Appl1
5	1719.6	97.4	2426	3 US-08-998-443-3	Sequence 3, Appl1
6	1719.6	97.4	2426	4 US-09-060-523-3	Sequence 3, Appl1
7	1661.2	94.1	2420	1 US-08-330-123A-3	Sequence 3, Appl1
8	1661.2	94.1	2420	4 US-09-580-517-3	Sequence 3, Appl1
9	1640.8	93.0	2425	2 US-08-485-778-1	Sequence 1, Appl1
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ALIGNMENTS

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; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-482-115B-3

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Query Match          97.4%; Score 1719.6; DB 1; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 AGCTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCCGGGAGGAGAGTTGACAGT 60
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DB 662 AGCTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCCGGGAGGAGTTGACAGT 720
    |||||

QY 61 AGCGAANTACGCGCAGTACAGTCCATCCAGCCCTGGCGGAAAGCAAGACTCCGTCTCA 120
    |||||
DB 721 AGCGAANTACGCGCAGTACAGTCCATCCAGCCCTGGCGGAAAGCAAGACTCCGTCTCA 780
    |||||

QY 121 AAAAAAAAAATCGTTACATTTATGTGATTTACTCCCTCTTTTACATCAACAGCA 180
    |||||
DB 781 AAAAAAAAAATCGTTACATTTATGTGATTTACTCCCTCTTTTACATCAACAGCA 840
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QY 181 CAGACTACTTTTAAAGCAAGTCAATATTTGAAGCGCTTTCTTCTTAATTAAGGAG 240
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DB 841 CAGACTACTTTTAAAGCAAGTCAATATTTGAAGCGCTTTCTTCTTAATTAAGGAG 900
    |||||

QY 241 ATTTCAGTCTTAAAGATTATATGATTTACATTTGATTTAAAGCATCTCTCTCA 300
    |||||
DB 901 ATTTCAGTCTTAAAGATTATATGATTTACATTTGATTTAAAGCATCTCTCTCA 960
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QY 301 AGGAGAAAGTTGAGAGAGCATTTCTAAGGAAAAAGGGGAGGTTGAACTCGAGCATC 360
    |||||
DB 961 AGGAGAGGCTGAGAGAGCATTTCTAAGGAAAAAGGGGAGGTTGAACTCGAGCATC 1020
    |||||

QY 361 CCAGTGGCGGAGACAGATTTCTGCTAGTCAAGTGTGCTGGGAAATCTATTTTCAAA 420
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DB 1021 CCAGTGGCGGAGACAGATTTCTGCTAGTCAAGTGTGCTGGGAAATCTATTTTCAAA 1080
    |||||

QY 421 AGTTTCCTCAAAAAATGTGATGATCAAAACTAGAAATAGTGTCTGATTTAGGCCCTA 480
    |||||
DB 1081 AGTTTCCTCAAAAAATGTGATGATCAAAACTAGAAATAGTGTCTGATTTAGGCCCTA 1140
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QY 481 AATTCCTCTGTAATTTCCATTTTAAAGTAGTCAAGTGAACCGGCTGTGCTCAGA 540
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DB 1141 AATTCCTCTGTAATTTCCATTTTAAAGTAGTCAAGTGAACCGGCTGTGCTCAGA 1200
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QY 541 GGATAGAAAAAGGCGCTGTGATACCTCAAGTTAGTTTCCCTTAAAGAGTCCGGAG 600
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DB 1201 GGATAGAAAAAGGCGCTGTGATACCTCAAGTTAGTTTCCCTTAAAGAGTCCGGAG 1260
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QY 601 TAAAGAGCAAGCCCTTCCCGGAGCTGGGAGGCAAGCTCTTCTCATGAGCCGGA 660
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DB 1261 TAAAGAGCAAGCCCTTCCCGGAGCTGGGAGGCAAGCTCTTCTCATGAGCCGGA 1320
    |||||

QY 661 ATGAGACTTAAATTTCCCGTCCCGCCCAACAGCCCGCGGAGAGTCACTCTCAGAG 720
    |||||
DB 1321 ATGAGACTTAAATTTCCCGTCCCGCCCAACAGCCCGCGGAGAGTCACTCTCAGAG 1380
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QY 721 AGCCGCGAGAGTACGCTTGCCCAATCCGTCGCGTGGCGGCGCTTCTTAAAGCGGA 780
    |||||
DB 1381 AGCCGCGAGAGTACGCTTGCCCAATCCGTCGCGTGGCGGCGCTTCTTAAAGCGGA 1440
    |||||

QY 781 CTGCGCCGCGAGCGACCGCGGTTGGGAGGTTGGGCGGAGGAGTGGTGGCAATTTT 840
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DB 1441 CTGCGCCGCGAGCGACCGCGGTTGGGAGGTTGGGCGGAGGAGTGGTGGCAATTTT 1500
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QY 841 TGTCTAACCTTAAGTGAAGAGGCGTGAAGCGCGCTTCTTCTCTCCCGCGGCTTTT 900
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DB 1501 TGTCTAACCTTAAGTGAAGAGGCGTGAAGCGCGCTTCTTCTCTCCCGCGGCTTTT 1560
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QY 901 TGTCTGCTGACTTTCAGCGGCGGAAAAAGCTCGGCTCGCGCTTCCACCTGTTCAATTA 960
    |||||
DB 1561 TGTCTGCTGACTTTCAGCGGCGGAAAAAGCTCGGCTCGCGCTTCCACCTGTTCAATTA 1620
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QY 961 GAGCAAAACAAAAATGTCAAGTGTGCGGCTTCCCGCGGAGACTCGGCGGCT 1020
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DB 1621 GAGCAAAACAAAAATGTCAAGTGTGCGGCTTCCCGCGGAGACTCGGCGGCT 1680
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QY 1021 GCGCTGCGCCAGCGCCCGGAACCCCGCTGAGAGCGCGGCTCGGCGGCTTCTCCGAG 1080
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DB 1741 GCACCTACTGCGCACCGGAGAGTTGGGCTCTCTCAAGCGCGGCTCTCTCGGCGGAG 1800
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QY 1140 GCGAGTTCAAGGCTTTCAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199
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DB 1801 GCGAGTTCAAGGCTTTCAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
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QY 1200 CGATTCCTGAGCTGTGGGAGCGTCAAGCCAGAGCTGGGCTCACACTGAGTTGCTTTC 1259
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DB 1861 CGATTCCTGAGCTGTGGGAGCGTCAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
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QY 1260 CTGTTGGTGGGAGAGCGGATCGTCCATCCGATCCGCTCGCGCGGAGTGGGAGCT 1319
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DB 1921 CTGTTGGTGGGAGAGCGGATCGTCCATCCGATCCGCTCGCGCGGAGTGGGAGCT 1980
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QY 1320 TGTGAACCCCAACTGACTGACTGCGCAGTGTGCTCAAAATTTGCGAGAGAGTGA 1379
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DB 1981 TGTGAACCCCAACTGACTGACTGCGCAGTGTGCTCAAAATTTGCGAGAGAGTGA 2040
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QY 1380 GGCACCTCCAAAGTCGGCCAAATGAATGGGAGTGAAGCGGCGTTCCTGGAGCGCTTC 1439
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DB 2041 GGCACCTCCAAAGTCGGCCAAATGAATGGGAGTGAAGCGGCGTTCCTGGAGCGCTTC 2100
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QY 1440 CTGCGTGGGTTCTCCGCTTCCGCTTTTGTGCTTATATGTTGATTTCAACTTAA 1499
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DB 2101 CTGCGTGGGTTCTCCGCTTCCGCTTTTGTGCTTATATGTTGATTTCAACTTAA 2160
    |||||

QY 1500 TTCCGCTCTGAGATTTGTGAGGTTTGTGCTTCTCCAGAGTGAATCTGACACTG 1559
    |||||
DB 2161 TTCCGCTCTGAGATTTGTGAGGTTTGTGCTTCTCCAGAGTGAATCTGACACTG 2220
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QY 1560 CCCTCAACGGGGGTGGGAGAGAGTCAATTTTGTGAGATCAATTTAACTTAAATG 1619
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DB 2221 CCCTCAACGGGGGTGGGAGAGAGTCAATTTTGTGAGATCAATTTAACTTAAATG 2280
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QY 1620 AATATTTAATTTAGAGATTTAATGAACATTTGGAATTTGCTCTTAAATGTCATCG 1679
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DB 2341 TTTATGCGAGAGTGAAGTTCTTTTGAATAATTAAGACTTGGGAGTGAACCTTGA 2400
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QY 1740 CAGTAGGATATAACCCCAAGCTT 1765
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DB 2401 CAGTAGGATATAACCCCAAGCTT 2426
    |||||

RESULT 2
US-08-660-678A-3
; Sequence 3, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villefontaine, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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Db 2341 TTTATGCCAGAGGTGAGAGTTCTTTTGAANAATAGACCTTGGGATGACCTTGAG 2400
QY 1740 CAGTAGGATATATACCCCGCAGACTT 1765
Db 2401 CAGTAGGATATATACCCCGCAGACTT 2426

RESULT 3
US-08-472-802C-4
; Sequence 4, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-472-802C-4

Query Match 97.4%; Score 1719.6; DB 2; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 AGTACTCAGGAGGCTGAGACACGAGATCGCTTAACCCGGGAGCAGAGTTGCAGTG 60
Db 662 ACCTACTCGAGGGCTGAGACACGAGAAATCGCTTGAACCCGGGA-GCAGAGTTGCAGTG 720
QY 61 AGCCGAGATCAGCCACTAGACTCATCCAGCCTGGGGAAAGCAGAGACTCCGTCGA 120
Db 721 ACCCGAGATCAGCCACTAGACTCATCCAGCCTGGGGAAAGCAGAGACTCCGTCGA 780
QY 121 AAAAAAATGTTACATTTATGGTGATTAATCTCCCTTTTAACTCATCAAGACA 180
Db 781 AAAAAAATGTTACATTTATGGTGATTAATCTCCCTTTTAACTCATCAAGACA 840
QY 181 CAGCAGTCTTAAAGCAAGTCATGATGAACGCCCTTCTTCTTAATAAAGGAG 240
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Db 841 CAGCAGTCTTAAAGCAAGTCATGATGAACGCCCTTCTTCTTAATAAAGGAG 900
QY 241 ATTAGTCTTAAAGTAAATATGATAGTACTTACACTTGATTAAGCCATCTCTGTCA 300
Db 901 ATTGAGTCTTAAAGTAAATATGATAGTACTTACACTTGATTAAGCCATCTCTGTCA 960
QY 301 AGGAGAGCTGAGAGAGGCAATTTAAGSAAAAAGGGGCGAGGTTGAACTCGGACGATC 360
Db 961 AGGAGAGCTGAGAGAGGCAATTTAAGSAAAAAGGGGCGAGGTTGAACTCGGACGATC 1020
QY 361 CCACTAGCCGAGACAAGATTCGTGTAGTCAAGTCTGCTGGAATCTATTTTCAAA 420
Db 1021 CCACTAGCCGAGACAAGATTCGTGTAGTCAAGTCTGCTGGAATCTATTTTCAAA 1080
QY 421 AGTTCTCAAAAAATGATGATCAAACTAGCAATTAATGTTCTGTCTTAAAGCCCTA 480
Db 1081 AGTTCTCAAAAAATGATGATCAAACTAGCAATTAATGTTCTGTCTTAAAGCCCTA 1140
QY 481 AATCTCTGTGAATTCATTTTAAAGTATGAGTGAAGCCGCTGTGTGCGAGA 540
Db 1141 AATCTCTGTGAATTCATTTTAAAGTATGAGTGAAGCCGCTGTGTGCGAGA 1200
QY 541 GGAATGAAAAAGGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGTCGAG 600
Db 1201 GGAATGAAAAAGGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGTCGAG 1260
QY 601 TAAAGCCGAAAGCCTTCCCGAGAGTGGGAAAGGCGCAAGCTCTCTCTATGCGCGAA 660
Db 1261 TAAAGCCGAAAGCCTTCCCGAGAGTGGGAAAGGCGCAAGCTCTCTCTATGCGCGAA 1320
QY 661 ATGGAACCTTAAATTTCCGTTCCCGCAACAGCCCGCCGAGAGTGAATCTCAAG 720.
Db 1321 ATGGAACCTTAAATTTCCGTTCCCGCAACAGCCCGCCGAGAGTGAATCTCAAG 1380
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Db 1381 AGCCGAGAGTCAAGCTTGGCCAAATCCGTGGGCGGCGCGCTTCTTATTAAGCCGA 1440
QY 781 CTGCGCCGCGAGCGCAGCGGTTCCGAGGCGTGGAGAGGCGTGGCCATTTT 840
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QY 1021 CGCCTGCCAGCCCGGAAACCCGCGTGAAGCGCGGCGTCCGCGGCTTCTCCGGAG 1080
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QY 1081 GCACCTAATGCGCACCGGAAAGATT-GGCTCTGTCAAGCCGCGGCTCTCGGGGCGAG 1139
Db 1741 GCACCTAATGCGCACCGGAAAGATTGGGCTGTGTCAAGCCGCGGCTCTCGGGGCGAG 1800
QY 1140 GCGAGGTTAGGCTTTCAGAGCGCGAGAAAGGAAAGGAGGAGTATCCCGCGCGCGG 1199
Db 1801 GCGAGGTTAGGCTTTCAGAGCGCGAGAAAGGAGGAGGAGTATCCCGCGCGCGG 1860
QY 1200 CGATTCCTTGAGCTGTGGAAGTGAACCCAGAGACTCGGCTCAACATGACATGCTTTC 1259
Db 1861 CGATTCCTTGAGCTGTGGAAGTGAACCCAGAGACTCGGCTCAACATGACATGCTTTC 1920
QY 1260 CTGTTGCTGGGGGAAGCGCGATCGTGGCGATCGCTCAACCCCTCGCGCGAGTGGGCT 1319
Db 1921 CTGTTGCTGGGGGAAGCGCGATCGTGGCGATCGCTCAACCCCTCGCGCGAGTGGGCT 1980
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QY 1320 TGTGAACCCCAACCTGACTGACGTGGCCAGTGTCTGCAAAATTGGCAGAGACCTGAA 1379
1981 TGTGAACCCCAACCTGACTGACGTGGCCAGTGTCTGCAAAATTGGCAGAGACCTGAA 2040
QY 1380 GGCACCTCCAAAGTGGCCCAAAATGAATGGCAGTACCGGGGTTGCTGAGCCGTTTC 1439
2041 GGCACCTCCAAAGTGGCCCAAAATGAATGGCAGTACCGGGGTTGCTGAGCCGTTTC 2100
QY 1440 CTGCGTGGGTCTCCGCTGCTCCGCTTTTGTGCTTATGCTGTATTAACCTTGA 1499
2101 CTGCGTGGGTCTCCGCTGCTCCGCTTTTGTGCTTATGCTGTATTAACCTTGA 2160
QY 1500 TTCCCTGCTGCAAGATTTTGTGAGGTTTGTCTCTCCAAAGTGAATCTGACACAGTC 1559
2161 TTCCCTGCTGCAAGATTTTGTGAGGTTTGTCTCTCCAAAGTGAATCTGACACAGTC 2220
QY 1560 CCTCAACGGGGTGTGGGAGACATGATTTTTTTTGAAGATCATTTAATTAATG 1619
2221 CCTCAACGGGGTGTGGGAGACATGATTTTTTTTGAAGATCATTTAATTAATG 2280
QY 1620 AATATTAAATGAAGATCTAAATGAACATTTGAATGTGCTTAAATGCTCATCGG 1679
2281 AATATTAAATGAAGATCTAAATGAACATTTGAATGTGCTTAAATGCTCATCGG 2340
QY 1680 TTATCCAGAGGTTGAAGTTCTTTTGAATAATAGACCTTGGCATGACCTTGA 1739
2341 TTATCCAGAGGTTGAAGTTCTTTTGAATAATAGACCTTGGCATGACCTTGA 2400
Db 1740 CAGTAGGATTAACCCCAACAGCTT 1765
QY 2401 CAGTAGGATTAACCCCAACAGCTT 2426

RESULT 4

US-08-714-482-1
Sequence 1, Application US/08714482
Patent No. 5972605
GENERAL INFORMATION:
APPLICANT: Villefontaine, Bryant
APPLICANT: Harley, Calvin
TITLE OF INVENTION: Assays for Regulators of Mammalian
NUMBER OF SEQUENCES: 2
TITLE OF INVENTION: Telomerase Expression
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,482
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/521,634
FILING DATE: 31-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0086005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..2426 /note="Sauli-HindIII fragment
OTHER INFORMATION: containing hmr sequences as well as
OTHER INFORMATION: transcription regulatory sequences"
US-08-714-482-1

Query Match 97.4%; Score 1719.6; DB 2; Length 2426;
Best local similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 AGCTACTCAGAGAGGCTGAGACACGAGAAATCGTTGAACCCGGGAGCAGAGTTGCAATG 60
Db 662 AGCTACTCAGAGAGGCTGAGACACGAGAAATCGTTGAACCCGGGAGCAGAGTTGCAATG 720
QY 61 AGCGGATCAGCGGCTGAGACACGAGAAATCGTTGAACCCGGGAGCAGAGTTGCAATG 120
Db 721 AGCGGATCAGCGGCTGAGACACGAGAAATCGTTGAACCCGGGAGCAGAGTTGCAATG 780
QY 121 AAAAAAATCGTTGCAATTTATGTTGATTTACTCCCTCTTTTACCTCATCAAGACA 180
Db 781 AAAAAAATCGTTGCAATTTATGTTGATTTACTCCCTCTTTTACCTCATCAAGACA 840
QY 181 CAGCACTACTTTAAAGCAAAATGATTTGAAGAGCCCTTTCTTCTAATAAAGGAG 240
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Db 901 ATTCACTCCTTAAGTAAATTAATGATTTAGTACTGATTTAAAGCAATCCTCTGCTCA 960
QY 301 AGGAGAGCTGAGAGAGCATTTCTAAGAGAAAAAGGGGAGGTTGGAACTCGGAGCATC 360
Db 961 AGGAGAGCTGAGAGAGCATTTCTAAGAGAAAAAGGGGAGGTTGGAACTCGGAGCATC 1020
QY 361 CCAGTAGCCGAGACAAAGATTTGCTGTAGTCAGTCTGCTGGGAATCTATTTCACAA 420
Db 1021 CCAGTAGCCGAGACAAAGATTTGCTGTAGTCAGTCTGCTGGGAATCTATTTCACAA 1080
QY 421 AGTTTCACAAAAATGATGATCAAAACCTAGGAATTAAGTTGCTGTCTTAAGGCCCA 480
Db 1081 AGTTTCACAAAAATGATGATCAAAACCTAGGAATTAAGTTGCTGTCTTAAGGCCCA 1140
QY 481 AATCTTCTGTGAATTCATTTTAAAGTAGTCAGAGTGAACCCGCTGTGCTCACA 540
Db 1141 AATCTTCTGTGAATTCATTTTAAAGTAGTCAGAGTGAACCCGCTGTGCTCACA 1200
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QY 661 ATGGAACCTTAATTTCCGCTCCGCCCAACAGCCGCCGAGAGAGTACTCTACAGAG 720

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Db      2401 CAGTAGATATACCCCGCACAGCTT 2426

RESULT 5
US-08-998-443-3
; Sequence 3, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
;   APPLICANT: Villeponteau, Bryant
;   APPLICANT: Peng, Junli
;   APPLICANT: Funk, Walter
;   APPLICANT: Andrews, William H.
;   TITLE OF INVENTION: Mammalian Telomerase
;   NUMBER OF SEQUENCES: 30
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, Eighth Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/998,443
;     FILING DATE:
;   CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/08/660,678
;       FILING DATE: 05-JUN-1996
;       APPLICATION NUMBER: US 08/330,123
;       FILING DATE: 27-OCT-1994
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/272,102
;         FILING DATE: 07-JUL-1994
;         ATTORNEY/AGENT INFORMATION:
;           NAME: Storella, John R.
;           REGISTRATION NUMBER: 32,944
;           REFERENCE/DOCKET NUMBER: 015389-00081IUS
;           TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;           INFORMATION FOR SEQ ID NO: 3:
;             SEQUENCE CHARACTERISTICS:
;               LENGTH: 2426 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;             MOLECULE TYPE: DNA (genomic)
;   US-08-998-443-3

Query Match      97.4%; Score 1719.6; DB 3; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

OY      1 ACTCTCTGAGGAGGGGTGAGACACAGAGATCGTTGACCCGGGAGGACAGAGTTCACAGT 60
Db      662 AGCTACTCTGAGGAGGGGTGAGACACAGAGAAATCGTTGAACCCCGGA-GCAGAGGTTTCAAGCA 720

OY      61 AGCCGAGATCAGCCACATAGACTCCATCCATCCAGCTGGGGAAGAGACAGACATCGCTCTCA 120
Db      721 AGCCGAGATCAGCCACATAGACTCCATCCATCCAGCTGGGGAAGAGACAGACTCGCTCTCA 780

OY      121 AAAAAAATCGTTACATTTATGCTGATTTACTCCCTCTTTTACCTCATCAAGACA 180
Db      781 AAAAAAATCGTTACATTTATGCTGATTTACTCCCTCTTTTACCTCATCAAGACA 840

OY      181 CAGCAGCTTTAAAGCAAGTCATGTTGAAGCGCTTTCTTCTTAATAAAAAGGAG 240
Db      841 CAGCAGCTTTAAAGCAAGTCATGTTGAAGCGCTTTCTTCTTAATAAAAAGGAG 900

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Qy	241	ATTGAGTCCTTAAGATTAAATGATAGTGTAGTACATCTGATTAAGAAAGCATCCTGCTGCA	300
Db	901	ATTGAGTCCTTAAGATTAAATGATAGTGTAGTACATCTGATTAAGAAAGCATCCTGCTGCA	960
Qy	301	AGGAGAAGCTGGAGAAAGCATTTCTTAAGGAAAAAGGGGCAAGGTTTGAATCTGGAGCATC	360
Db	961	AGGAGAAGCTGGAGAAAGCATTTCTTAAGGAAAAAGGGGCAAGGTTTGAATCTGGAGCATC	1020
Qy	361	CCACTGAGCCGAGACAMGATTCGTCGTGTAGTCAAGTCTCCTCGGGAAATCTATTTCACAA	420
Db	1021	CCACTGAGCCGAGACAMGATTCGTCGTGTAGTCAAGTCTCCTCGGGAAATCTATTTCACAA	1080
Qy	421	AGTTCTCCAAAAAATGTGATGATCAAAACATAGGAATTAAGTTCTGTCTTAAAGCCCTA	480
Db	1081	AGTTCTCCAAAAAATGTGATGATCAAAACATAGGAATTAAGTTCTGTCTTAAAGCCCTA	1140
Qy	481	AAATCTTCTGTGANTCCATTTTAAAGGTAGTCGAGGTGAACCGCTCTGTGTGACA	540
Db	1141	AAATCTTCTGTGANTCCATTTTAAAGGTAGTCGAGGTGAACCGCTCTGTGTGACA	1200
Qy	541	GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTACCTTAAAGAAAGGTCGGAG	600
Db	1201	GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTACCTTAAAGAAAGGTCGGAG	1260
Qy	601	TAAAGACGCAAAAGCCTTCCCGAGCGTGGCGAAGGCAACGTCCTTCCATAGGCCGGA	660
Db	1261	TAAAGACGCAAAAGCCTTCCCGAGCGTGGCGAAGGCAACGTCCTTCCATAGGCCGGA	1320
Qy	661	ATGGAATCTTAATTTTCCCGTTCCCGCCCAACAGACCCGCGGAGAGATGACTCTAGAG	720
Db	1321	ATGGAATCTTAATTTTCCCGTTCCCGCCCAACAGACCCGCGGAGAGATGACTCTAGAG	1380
Qy	721	AGCGCGAGAGTCACTTTGGCCCAATCGTAGCGGTGGCGCGCGCTCTTAAAGCCGA	780
Db	1381	AGCGCGAGAGTCACTTTGGCCCAATCGTAGCGGTGGCGCGCGCTCTTAAAGCCGA	1440
Qy	781	CTGCGCCGCGCAAGCGCACCGGGTTGGCGAGGGTGGCTTGGAGGGGTGGTGGCCATTTTT	840
Db	1441	CTGCGCCGCGCAAGCGCACCGGGTTGGCGAGGGTGGCTTGGAGGGGTGGTGGCCATTTTT	1500
Qy	841	TGTGTAAACCTTAACCTGGAAGGGCGTAGAGCGCGTCTTTTCTCTCCCGCGCGCTTTT	900
Db	1501	TGTGTAAACCTTAACCTGGAAGGGCGTAGAGCGCGTCTTTTCTCTCCCGCGCGCTTTT	1560
Qy	901	TCTGCTGACTTTCAGCGGGCGGAAAAAGCCTCGCGCTTCGCGCTTCAACCTTCACTTA	960
Db	1561	TCTGCTGACTTTCAGCGGGCGGAAAAAGCCTCGCGCTTCGCGCTTCAACCTTCACTTA	1620
Qy	961	GAGCAAAACAAAAAATGTCACTCTGTGGCCCTGTCCCGGGGACCTGCGCGCGGT	1020
Db	1621	GAGCAAAACAAAAAATGTCACTCTGTGGCCCTGTCCCGGGGACCTGCGCGCGGT	1680
Qy	1021	CGCGTCCCAACCCCGCAACCCCGCTGGAAGGGCGGGGTCTTCCGAG	1080
Db	1681	CGCGTCCCAACCCCGCAACCCCGCTGGAAGGGCGGGGTCTTCCGAG	1740
Qy	1081	GCACCTACTGCAACCGCGAAGATT--GGCTCTGTCAAGCGGCGTCTTCTGGGGCGAG	1139
Db	1741	GCACCTACTGCAACCGCGAAGATT--GGCTCTGTCAAGCGGCGTCTTCTGGGGCGAG	1800
Qy	1140	GGGAGGTTCAAGGCTTTCAGCGCGGCGAGAAAGAAAGAAAGGAGGACTTCCCGCGCGGCG	1199
Db	1801	GGGAGGTTCAAGGCTTTCAGCGCGGCGAGAAAGAAAGAAAGGAGGACTTCCCGCGCGGCG	1860
Qy	1200	CGATTCCCTAGCTGTGTGGAGCTGCAACCCAGGACTGTGCTCAACATGCAATGATTCGTTTC	1259
Db	1861	CGATTCCCTAGCTGTGTGGAGCTGCAACCCAGGACTGTGCTCAACATGCAATGATTCGTTTC	1920
Qy	1260	CTGTGTGGTGGGGGAAGCGCGATCTGTGTGCGATCTCGTACACCTCTCGCGCGCACTGGGGCT	1319
Db	1921	CTGTGTGTGGGGGAAGCGCGATCTGTGTGCGATCTCGTACACCTCTCGCGCGCACTGGGGCT	1980

QY	1330	TGTAAACCCCAAAACGACGTGACTGGGACAGTGTCTGCAAAATTGGCAGAGACGTGAA	1379
Db	1981	TGTAAACCCCAAAACGACGTGACTGGGACAGTGTCTGCAAAATTGGCAGAGACGTGAA	2040
QY	1380	GGCACCTCCAAAGTCGGCCAAATGATGGGCAGTGAAGCCGGGGTTCCTGTGAGCCGTTTC	1439
Db	2041	GGCACCTCCAAAGTCGGCCAAATGATGGGCAGTGAAGCCGGGGTTCCTGTGAGCCGTTTC	2100
QY	1440	CTGGGTGGGTCTCCGCTCTCCGCTTTTGTGTGCCTTTATGTTGTTATTCACACTTAG	1499
Db	2101	CTGGGTGGGTCTCCGCTCTCCGCTTTTGTGTGCCTTTATGTTGTTATTCACACTTAG	2160
QY	1500	TTCCCTGCTGCAGATTTTGTGAGTTTTGTCTCCCAAGATGAGATCTGCAGACATC	1559
Db	2161	TTCCCTGCTGCAGATTTTGTGAGTTTTGTCTCTCCCAAGATGAGATCTGCAGACATC	2220
QY	1560	CCCTCAACGGGGTGTGGGACACATCTATTTTTTTTGAGAGATCATTTACATTTAATG	1619
Db	2221	CCCTCAACGGGGTGTGGGACACATCTATTTTTTTTGAGAGATCATTTACATTTAATG	2280
QY	1620	AATATTAAATTAGAGAGATCTAAATGAAACATGTGAAATGTGTCCCTTAATGTCATGG	1679
Db	2281	AATATTAAATTAGAGAGATCTAAATGAAACATGTGAAATGTGTCTTTAATGTCATGG	2340
QY	1680	TTTATGCGAGAGGTTAGAAATTTCTTTTGTGAAAAATTAGACCTTGGCGATGACCTTAG	1739
Db	2341	TTTATGCGAGAGGTTAGAAATTTCTTTTGTGAAAAATTAGACCTTGGCGATGACCTTAG	2400
QY	1740	CAGTAGGATATACCCCAACACTT	1765
Db	2401	CAGTAGGATATACCCCAACACTT	2426

RESULT 6
 US-09-060-523-3
 Sequence 3, Application US/09060523
 Patent No. 6258535
 GENERAL INFORMATION:
 APPLICANT: Villeponteau, Bryant
 APPLICANT: Feng, Junli
 APPLICANT: Funk, Walter
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Mammalian Telomerase
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/060,523
 FILING DATE: 14-APR-1998
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/660,678
 FILING DATE: 05-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/330,123
 FILING DATE: 27-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/272,102
 FILING DATE: 07-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 REFERENCE/DOCKET NUMBER: 015389-000813US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-060-523-3

Query Match 97.4%; Score 1719.6; DB 4; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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OY 1 AGCTCTGAGAGGGGTGAGACACGAAATGCTTGAAACCCGGGAGGACAGAGTTCAGTG 60
Db 662 AGCTACTAGAGGGGTGAGACACGAAATGCTTGAAACCCGGGAGGACAGAGTTCAGTG 720
OY 61 AGCCGAGATCAGCCACTAGACTCCATCCAGCCCTGGGGGAAAGCAAGACTCCGTCTCA 120
Db 721 AGCCGAGATCAGCCACTAGACTCCATCCAGCCCTGGGGGAAAGCAAGACTCCGTCTCA 780
OY 121 AAAAAAAAAATGTTACAAATTTATGTTGATTTACTCCCTCTTTTACCTCATCAAGACA 180
Db 781 AAAAAAAAAATGTTACAAATTTATGTTGATTTACTCCCTCTTTTACCTCATCAAGACA 840
OY 181 CAGCACTACTTTAAGCAAAATGATTTGAAGCCGCTTTCTTTCTAATAAAGGAG 240
Db 841 CAGCACTACTTTAAGCAAAATGATTTGAAGCCGCTTTCTTTCTAATAAAGGAG 900
OY 241 ATTGAGTCTTAAATTAATGATTTAGTTAGTTACTTACTTGAATTAAGCATCTCTGCTCA 300
Db 901 ATTGAGTCTTAAATTAATGATTTAGTTAGTTACTTACTTGAATTAAGCATCTCTGCTCA 960
OY 301 AGGAGAGCTGAGAGAGCAATTCATAAGSAAAGGAGGAGGTTGAACTCGAGCATC 360
Db 961 AGGAGAGCTGAGAGAGCAATTCATAAGSAAAGGAGGAGGTTGAACTCGAGCATC 1020
OY 361 CCAGTACGCCGAGACAGATTCGTGTAGTCAAGTCTGCTGGGAATCATTTTTCAGAA 420
Db 1021 CCAGTACGCCGAGACAGATTCGTGTAGTCAAGTCTGCTGGGAATCATTTTTCAGAA 1080
OY 421 AGTTCTCCAAAAATGATGATCAAACTAGAAATTTAGTTCTGTGTCTTAAAGCCCTA 480
Db 1081 AGTTCTCCAAAAATGATGATCAAACTAGAAATTTAGTTCTGTGTCTTAAAGCCCTA 1140
OY 481 AAATCTTCTGTGAATTCATTTTAAAGTAGTCGAGTGAACCCGGTCTGCTGAGCA 540
Db 1141 AAATCTTCTGTGAATTCATTTTAAAGTAGTCGAGTGAACCCGGTCTGCTGAGCA 1200
OY 541 GGTATACAAAAAGGCGCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAAAGTCGAG 600
Db 1201 GGTATACAAAAAGGCGCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAAAGTCGAG 1260
OY 601 TAAAGACGCAAGCCCTTCCGAGAGTGGCGAAGGCAACGCTCTCTCATGGCCGGA 660
Db 1261 TAAAGACGCAAGCCCTTCCGAGAGTGGCGAAGGCAACGCTCTCTCATGGCCGGA 1320
OY 661 ATGGAATTTAATTTCCGCTTCCGCCCAACAGCCGCCCGAGAGATGATCTCAGAG 720
Db 1321 ATGGAATTTAATTTCCGCTTCCGCCCAACAGCCGCCCGAGAGATGATCTCAGAG 1380
OY 721 AGCCGAGAGATCAGCTTGGCCAAATCGTGCGGTGGGGCGCCGCTCCCTTTAATAAGCGA 780
Db 1381 AGCCGAGAGATCAGCTTGGCCAAATCGTGCGGTGGGGCGCCGCTCCCTTTAATAAGCGA 1440
OY 781 CTCGCCCGGACAGCCAGCGGTGGCGAGAGTGGGCTGGGAGGAGGTGGCATTTT 840
Db 1441 CTCGCCCGGACAGCCAGCGGTGGCGAGAGTGGGCTGGGAGGAGGTGGCATTTT 1500
OY 841 TGTCTAACCTTAACGAGAGGCGGTAGGCGCCGCTCTTTTGTCTCCCGCGCGCTGTTTT 900
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Db 1501 TGTCTAACCTTAACGAGAGGCGGTAGGCGCCGCTCTTTTGTCTCCCGCGCGCTGTTTT 1560
OY 901 TCTGCTGACTTTTCAAGCGGGCGGAAAGCCCTGAGCTGCGGCTTCAACCGTTCAATTTCA 960
Db 1561 TCTGCTGACTTTTCAAGCGGGCGGAAAGCCCTGAGCTGCGGCTTCAACCGTTCAATTTCA 1620
OY 961 GAGCAAAACAAAAATGTCAGCTGCTGCTGCGGCTTCCGCCGAGACCTGCGCGGGGT 1020
Db 1621 GAGCAAAACAAAAATGTCAGCTGCTGCTGCGGCTTCCGCCGAGACCTGCGCGGGGT 1680
OY 1021 CGCCTGCCAGCCGCCGGAACCCCGCTGAGAGCCGCGGAGCCGCGGAGCTTCTCCGAG 1080
Db 1681 CGCCTGCCAGCCGCCGGAACCCCGCTGAGAGCCGCGGAGCCGCGGAGCTTCTCCGAG 1740
OY 1081 GCACCTTACTGCCAGCGCGGAAGATT-GGCTCTGTACGCCGCGGGTCTCTCGGGGCGAG 1139
Db 1741 GCACCTTACTGCCAGCGCGGAAGATTGGCTCTGTACGCCGCGGGTCTCTCGGGGCGAG 1800
OY 1140 GCGAGGTTGAGGCTTTTCAAGCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199
Db 1801 GCGAGGTTGAGGCTTTTCAAGCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
OY 1200 CGATTCCCTGAGCTGTGGAGCTGCACCCAGAGACTCGGCTCAGCATGAGTTGCTTTTC 1259
Db 1861 CGATTCCCTGAGCTGTGGAGCTGCACCCAGAGACTCGGCTCAGCATGAGTTGCTTTTC 1320
OY 1260 CTGTTGTGGGGGGAAGCCGATGCTGCGCATCCGCTACCCCTGCGCGGAGTGGGGCT 1319
Db 1921 CTGTTGTGGGGGGAAGCCGATGCTGCGCATCCGCTACCCCTGCGCGGAGTGGGGCT 1380
OY 1320 TGTGAACCCCAAACTGACTGAGTGGGCCAGTGTGCTGCAAAATGSCAGAGACGTGA 1379
Db 1981 TGTGAACCCCAAACTGACTGAGTGGGCCAGTGTGCTGCAAAATGSCAGAGACGTGA 2040
OY 1380 GGCACCTCCAAAGTCGGCAAAATGAATGGGCAATGAGCGGAGTTCCTGAGCCGTTTC 1439
Db 2041 GGCACCTCCAAAGTCGGCAAAATGAATGGGCAATGAGCGGAGTTCCTGAGCCGTTTC 2100
OY 1440 CTGCGTGGGTTCTCCGCTCTTCTGCTTGTGCTTATGAGTTATTAACCTTATG 1499
Db 2101 CTGCGTGGGTTCTCCGCTCTTCTGCTTGTGCTTATGAGTTATTAACCTTATG 2160
OY 1500 TTCTGCTGTCGACATTTTGTAGGTTTGTGCTTCTCCAGAGTATCTGACACGATC 1559
Db 2161 TTCTGCTGTCGACATTTTGTAGGTTTGTGCTTCTCCAGAGTATCTGACACGATC 2220
OY 1560 CCTTCAACGGGGTCTGGGAGACATTTTGTGAGAGATCTTTTAACATTTAATG 1619
Db 2221 CCTTCAACGGGGTCTGGGAGACATTTTGTGAGAGATCTTTTAACATTTAATG 2280
OY 1620 AATTTTAATTAAGATCTTAATTAATGAACATTTGGAATTTGTTTAAATGTCATGG 1679
Db 2281 AATTTTAATTAAGATCTTAATTAATGAACATTTGGAATTTGTTTAAATGTCATGG 2340
OY 1680 TTTATGCCAGAGTTTGAAGTTCTTTTGAAGAAATTTAGACCTTGGGATACCTTGA 1739
Db 2341 TTTATGCCAGAGTTTGAAGTTCTTTTGAAGAAATTTAGACCTTGGGATACCTTGA 2400
OY 1740 CAGTAGATTTAAACCCCAACAGCTT 1765
Db 2401 CAGTAGATTTAAACCCCAACAGCTT 2426
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RESULT 7
US-08-330-123A-3
Sequence 3, Application US/08330123A
Patent No. 5383016
GENERAL INFORMATION:
APPLICANT: VILLEPONTÉAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.

```

: TITLE OF INVENTION: HUMAN TELOMERASE
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/330,123A
: FILING DATE: 27-OCT-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/272,102
: FILING DATE: 07-JUL-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 15389-000810
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2420 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-330-123A-3

Query Match      94.1%; Score 1661.2; DB 1; Length 2420;
Best local similarity 98.5%; Pred. No. 0;
Matches 1740; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

QY      1 AGCTACTCAGGAGGCTGAGACACGAGAAATCGCTTGAACCCGGGAGGAGAGTGGAGTG 60
DB      662 AGCTACTCAGGAGGCTGAGACACGAGAAATCGCTTGAACCCGGGAGGAGAGTGGAGTG 720
QY      61 AGCGGATCAGCGCCACTGACTCCATCCACGCTGGGCGAAGAGCAAACTCCGCTCA 120
DB      721 AGCGGATCAGCGCCACTGACTCCATCCACGCTGGGCGAAGAGCAAACTCCGCTCA 780
QY      121 AAAAAAAAAATCGTATGATTTATGGTGAATTTACTCCCTTTTAACTCATCAAGACA 180
DB      781 AAAAAAAAAATCGTATGATTTATGGTGAATTTACTCCCTTTTAACTCATCAAGACA 840
QY      181 CAGCACTACTTTAAACCAAGTCAATGATTGAACGCCCTTTCTTCTAATAAAGGAG 240
DB      841 CAGCACTACTTTAAACCAAGTCAATGATTGAACGCCCTTTCTTCTAATAAAGGAG 900
QY      241 ATTCACTCCTTAAGTAAATGATGATGTTGATTTCACTTGAATTAACCATCCTCTGCTCA 300
DB      901 ATTCACTCCTTAAGTAAATGATGATGTTGATTTCACTTGAATTAACCATCCTCTGCTCA 960
QY      301 AGGAGAAGTGGAGAGGATTTCTAAGAAAAAGGGGAGGCTTGGAACTCGAGCGCATC 360
DB      961 AGGAGAAGTGGAGAGGATTTCTAAGAAAAAGGGGAGGAGGAGTGAAGCACTCGAGCGCATC 1020
QY      361 CCACCTAGCGCGAGACAAGATTCTGCTGTAGTCACTGCTGCTGGGAATCTATTTCACAA 420
DB      1021 CCACCTAGCGCGAGACAAGATTCTGCTGTAGTCACTGCTGCTGGGAATCTATTTCACAA 1080
QY      421 AGTTCTCAAAAAATGATGATCAAAACATGAGGAATTAGTGTCTGTGCTTGGGCGCTA 480
DB      1081 AGTTCTCAAAAAATGATGATCAAAACATGAGGAATTAGTGTCTGTGCTTGGGCGCTA 1140
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QY      481 AATCTCTGTGAATTCATTTTTAAGTAGTCGAGGTGAACCGCGCTGTGCTGCAGA 540
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QY      541 GGTATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAGAGGTGCGAAG 600
DB      1201 GGTATAGAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTAAGAGGTGCGAAG 1260
QY      601 TAAAGAGCAAGGCTTCCCGGAGGTGGGGAAGGGCAAGCTCCCTCATGCGCGGAA 660
DB      1261 TAAAGAGCAAGGCTTCCCGGAGGTGGGGAAGGGCAAGCTCCCTCATGCGCGGAA 1320
QY      661 ATGGAATTTAATTTCCCTTCCCGCAACCAAGCCCGCGGAGAGAGTACTCTCAAGAG 720
DB      1321 ATGGAATTTAATTTCCCTTCCCGCAACCAAGCCCGCGGAGAGAGTACTCTCAAGAG 1380
QY      721 AGCGCGAGAGTCAGCTTGGCCATCCGTCGGGTGCGGCGCGCTCTTTATTAAGCCGA 780
DB      1381 AGCGCGAGAGTCAGCTTGGCCATCCGTCGGGTGCGGCGCGCTCTTTATTAAGCCGA 1440
QY      781 CTCGCGCGGAGGAGCGACCGGGTTGGGAGGGTGGGCTGGAGAGGGTGGTGGCATTTT 840
DB      1441 CTCGCGCGGAGGAGCGACCGGGTTGGGAGGGTGGGCTGGAGAGGGTGGTGGCATTTT 1500
QY      841 TGTCTAACCTTAAGTGAAGGGCGTAGGCGCGCTTTTGTCTCCCGCGCGCTGTTT 900
DB      1501 TGTCTAACCTTAAGTGAAGGGCGTAGGCGCGCTTTTGTCTCCCGCGCGCTGTTT 1560
QY      901 TCTGCTGACTTTCAGCGGGCGGAAAAAGCTTGGCTGCGCGCTTCCACGTTCAATCTA 960
DB      1561 TCTGCTGACTTTCAGCGGGCGGAAAAAGCTTGGCTGCGCGCTTCCACGTTCAATCTA 1620
QY      961 GAGCAAAACAAAAATGCTAGCTGCTGCGCCGCTTCCCGGAGCTGCGGGGGT 1020
DB      1621 GAGCAAAACAAAAATGCTAGCTGCTGCGCCGCTTCCCGGAGCTGCGGGGGT 1678
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QY      1081 GCACCTACTGCGACCGCGAAGAGTT- GGCCTCTGTCAAGCCGCGGGTCTCTCGGGGCGAG 1139
DB      1738 GCACCTACTGCGACCGCGAAGAGTT- GGCCTCTGTCAAGCCGCGGGTCTCTCGGGGCGAG 1797
QY      1140 GCGAGGTTTCAAGGCTTCAAGCGCGCGGAGGAAAGGAGGAGGAGGAGGAGGAGG 1199
DB      1798 GCGAGGTTTCAAGGCTTCAAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1854
QY      1200 CGATTCCTGAGCTGTGGACGTCGACCCGAGACTGGGCTCACACATGCAATGCAATTCGCTTTC 1259
DB      1855 CGATTCCTGAGCTGTGGACGTCGACCCGAGACTGGGCTCACACATGCAATTCGCTTTC 1914
QY      1260 CTGTGTGGGGGGGGAAGCGCGGATCTGCGCATCCGTCACCCCTGCGCGGAGTGGGGCT 1319
DB      1915 CTGTGTGGGGGGGGAAGCGCGGATCTGCGCATCCGTCACCCCTGCGCGGAGTGGGGCT 1974
QY      1320 TGTGAACCCCGCAACCTGACTGACTGGGCGAGTGTCTGCAAAATTTGAGAGAGCTGAA 1379
DB      1975 TGTGAACCCCGCAACCTGACTGACTGGGCGAGTGTCTGCAAAATTTGAGAGAGCTGAA 2034
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DB      2035 GGCACCTCCAAAGTCGGCCAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2094
QY      1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTGTGGCTTTTATGCTTGTATTAACACTTAA 1499
DB      2095 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTGTGGCTTTTATGCTTGTATTAACACTTAA 2154
QY      1500 TTTCTGCTCTGAGAGATTTTGTGAGGTTTGTGCTTCCCAAGTGTGATCTGACACAGTC 1559
DB      2155 TTTCTGCTCTGAGAGATTTTGTGAGGTTTGTGCTTCCCAAGTGTGATCTGACACAGTC 2214
QY      1560 CCTCAACGGGGGTGGGAGACAGTCATTTTTTTTGAAGATCATTTTAACATTTAATG 1619
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Db 2215 CCTCAACGGGCTGTGGGAGAACAGTCATTTTGTGAGACATCTTTAAACATTTAAATG 2274
Qy 1620 AATATTTAATTAAGATCTAAATGACATGTGAAATGTGTCTTAAATGTCATCGG 1679
Db 2275 AATATTTAATTAAGATCTAAATGACATGTGAAATGTGTCTTAAATGTCATCGG 2334
Qy 1680 TTTATGCCAGAGGTGTGAAGTTCTTTTGAATAATGACCTGGGATACCTTGAG 1739
Db 2335 TTTATGCCAGAGGTGTGAAGTTCTTTTGAATAATGACCTGGGATACCTTGAG 2394
Qy 1740 CAGTAGATATTAACCCCAAGCTT 1765
Db 2395 CAGTAGATATTAACCCCAAGCTT 2420

RESULT 8
US-09-580-517-3
; Sequence 3, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; FUNK, Walter
; FENG, Junli
; ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,517
; FILING DATE: 25-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/330,123
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2420 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-580-517-3

Query Match 94.1%; Score 1661.2; DB 4; Length 2420;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1740; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

Qy 1 ACCTCTCAGGAGGCTGTGACACGAGATTCGTTGAACCCGAGGACAGAGTTGCAAGT 60
Db 662 ACCTCTCAGGAGGCTGTGACACGAGATTCGTTGAACCCGAGGACAGAGTTGCAAGT 720
Qy 61 AGCCGAGATCAGCCACTAGACTCATCCAGCTGGGGGAAAGCAAGACTCCGTCCTCA 120

Db 721 AGCCGAGATCAGCCACTAGACTCATCCAGCTGGGGGAAAGCAAGACTCCGTCCTCA 780
Qy 121 AAAAAAAAAATCGTTACATTTATGTGATTAATCTCCCTCTTTTACCTCATCAAGACA 180
Db 781 AAAAAAAAAATCGTTACATTTATGTGATTAATCTCCCTCTTTTACCTCATCAAGACA 840
Qy 181 CAGCACTACTTTTAAGCAAAATGATTAAGAGCCCTTTCTTCTCTATTAAGAGGAG 240
Db 841 CAGCACTACTTTTAAGCAAAATGATTAAGAGCCCTTTCTTCTCTATTAAGAGGAG 900
Qy 241 ATTCACTCTTTAAGATTAATATGATTAAGATTAAGATTAAGATTAAGATTAAGAT 300
Db 901 ATTCACTCTTTAAGATTAATATGATTAAGATTAAGATTAAGATTAAGATTAAGAT 960
Qy 301 AGGAGAGCTGTGAGAGGATTCCTAAGCAAAAAGGGGACAGGCTTGAACTCGAGCATC 360
Db 961 AGGAGAGCTGTGAGAGGATTCCTAAGCAAAAAGGGGACAGGCTTGAACTCGAGCATC 1020
Qy 361 CCAGTACGCGGAGACAAAGATTCGCTGTAGTCAAGTGTGCTGGGATCTATTTTCAACA 420
Db 1021 CCAGTACGCGGAGACAAAGATTCGCTGTAGTCAAGTGTGCTGGGATCTATTTTCAACA 1080
Qy 421 AGTTCTCCAAAAATGATGATTAATCAAAACCTAGCAATTAAGTGTCTGTAGCCCTTA 480
Db 1081 AGTTCTCCAAAAATGATGATTAATCAAAACCTAGCAATTAAGTGTCTGTAGCCCTTA 1140
Qy 481 AATCTCTCTGTGAATTCATTTTAAGTGTAGTGTGAAGCCGCTGTGTGCTGAGA 540
Db 1141 AATCTCTCTGTGAATTCATTTTAAGTGTAGTGTGAAGCCGCTGTGTGCTGAGA 1200
Qy 541 GGAATGAAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTTAAAGAGTCGAGAG 600
Db 1201 GGAATGAAAAAAGGCCCTGTGATACCTCAAGTTAGTTTACCTTTTAAAGAGTCGAGAG 1260
Qy 601 TAAAGACCAAAAGCCTTCCCGGAGCTGCGGAAGGAGAGCTCTCTCTATGCGCGGAA 660
Db 1261 TAAAGACCAAAAGCCTTCCCGGAGCTGCGGAAGGAGAGCTCTCTCTATGCGCGGAA 1320
Qy 661 ATGGAATTTTATTTTCCGTTTCCCGGAGAGCCGCGGAGAGAGTGTGATCTGACAGAG 720
Db 1321 ATGGAATTTTATTTTCCGTTTCCCGGAGAGCCGCGGAGAGAGTGTGATCTGACAGAG 1380
Qy 721 AGCCGAGAGATCAGCTTGGCCATTCGCTGCGGCTGCGGCGCCCTCTCTTATTAAGCCGA 780
Db 1381 AGCCGAGAGATCAGCTTGGCCATTCGCTGCGGCTGCGGCGCCCTCTCTTATTAAGCCGA 1440
Qy 781 CTCGCCGGGACGCGACCGGCTTGGGAGGAGTGGGCTGCGGAGGAGTGGGCTGATTTT 840
Db 1441 CTCGCCGGGACGCGACCGGCTTGGGAGGAGTGGGCTGCGGAGGAGTGGGCTGATTTT 1500
Qy 841 TGTCTAACCTTAAGTGAAGGCGTGAAGGCGCTGCTTGTGCTCCCGCGCGCTGTTTT 900
Db 1501 TGTCTAACCTTAAGTGAAGGCGTGAAGGCGCTGCTTGTGCTCCCGCGCGCTGTTTT 1560
Qy 901 TCTCGCTGACTTTCAAGGGGCGGAAAAAGCCTGAGCTTGGCGGCTTCAACCTTATTTCTA 960
Db 1561 TCTCGCTGACTTTCAAGGGGCGGAAAAAGCCTGAGCTTGGCGGCTTCAACCTTATTTCTA 1620
Qy 961 GAGCAAAACAAAAATGTCAAGTGTCTGCGGCTTCCCGGAGAGCTGCGGCGGCT 1020
Db 1621 GAGCAAAACAAAAATGTCAAGTGTCTGCGGCTTCCCGGAGAGCTGCGGCGGCT 1078
Qy 1021 CGCCTGCCAGCCCGGAAACCCGCTGAGAGCGCGGCTGCGGCGGCTTCTCGGAG 1080
Db 1679 CGCCTGCCAGCCCGGAAACCCGCTGAGAGCGCGGCTGCGGCGGCTTCTCGGAG 1737
Qy 1081 GCACCTACTGTCCAGCGCGAAGATTGAGCTTGTCAAGCGCGGCTTCTCGGAGGAG 1139
Db 1738 GCACCTACTGTCCAGCGCGAAGATTGAGCTTGTCAAGCGCGGCTTCTCGGAGGAG 1797
Qy 1140 GCGAGGTTAGGCTTTTCAAGCGCGGAGAGAGAGAGAGAGTCCCGCGCGGCGG 1199
Db 1798 GCGAGGTTAGGCTTTTCAAGCGCGGAGAGAGAGAGAGAGTCCCGCGCGGCGG 1854

1200 CGATTCCCTGAGCTGTGGGAGCGTGAACCCAGAGCTGGGCTCACACATGAGTTGGCTTC 1259
1855 CGATTCCCTGAGCTGTGGGAGCGTGAACCCAGAGCTGGGCTCACACATGAGTTGGCTTC 1914
1260 CTGTTGGTGGGGGGAACGCCGATCGTGGCATCCGTACCCCTCGCCGGCAGTGGGGCT 1319
1915 CTGTTGGTGGGGGGAACGCCGATCGTGGCATCCGTACCCCTCGCCGGCAGTGGGGCT 1974
1320 TGTGAACCCCAAACTGACTGACTGGGCCAGTGTGCTGCAAAATGGCAGAGAGCTGAA 1379
1975 TGTGAACCCCAAACTGACTGACTGGGCCAGTGTGCTGCAAAATGGCAGAGAGCTGAA 2034
1380 GGCACCTCCAAAGTGGGCAAAATGAAATGGGCGAGTGGGCGGGGTTGCTGGAGCCGCTTC 1439
2035 GGCACCTCCAAAGTGGGCAAAATGAAATGGGCGAGTGGGCGGGGTTGCTGGAGCCGCTTC 2094
1440 CTGCGTGGGTTCTCCGCTCTCCGCTTTTGTGCTTTTATGTTGATTTACACTTAG 1499
2095 CTGCGTGGGTTCTCCGCTCTCCGCTTTTGTGCTTTTATGTTGATTTACACTTAG 2154
1500 TTCTCTCTCTGCGAGTTTGTGAGTTTGTCTTCTCCCAAGGTAGATCTGACACAGTC 1559
2155 TTCTCTCTCTGCGAGTTTGTGAGTTTGTCTTCTCCCAAGGTAGATCTGACACAGTC 2214
1560 CCCTCAACGGGGTGTGGGAGAACAGTCAATTTTGTGAGAGATCAATTAACATTAATG 1619
2215 CCCTCAACGGGGTGTGGGAGAACAGTCAATTTTGTGAGAGATCAATTAACATTAATG 2274
1620 AATATTTAATTAAGATCAATTAATGAACATTTGTTCTTATATGCTCATCG 1679
2275 AATATTTAATTAAGATCAATTAATGAACATTTGTTCTTATATGCTCATCG 2334
1680 TTATATCCGAGAGTTTGAAGTTTCTTTTGAATAATTAAGACTTGGCGATGACTTGA 1739
2335 TTATATCCGAGAGTTTGAAGTTTCTTTTGAATAATTAAGACTTGGCGATGACTTGA 2394
1740 CAGTAGATTAACCCCAACAGCTT 1765
2395 CAGTAGATTAACCCCAACAGCTT 2420

RESULT 9
US-08-485-778-1
Sequence 1, Application US/08485778
Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhendu, Maria Antonia Biasco
APPLICANT: Villeneuve, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-485-778-1
Query Match
Best Local Similarity 98.4%; Score 1640.8; DB 2; Length 2425;
Matches 1742; Conservative 0; Mismatches 17; Indels 11; Gaps 8:
1 AGCTACTCAGGAGGCTGAGACAGAGAAATCGTTGAACCCGGGAGGCAAGTTCAGT 60
662 AGCTACTCAGGAGGCTGAGACAGAGAAATCGTTGAACCCGGGAGGCAAGTTCAGT 720
61 AGCCGAGATCAGCCCACTGACTTCATCCAGCCTGGGCGAAGAGCAAGACTCGTCTCA 120
721 AGCCGAGATCAGCCCACTGACTTCATCCAGCCTGGGCGAAGAGCAAGACTCGTCTCA 780
121 AAAAAAAATCGTTCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 180
781 AAAAAAAATCGTTCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 840
181 CAGCACTACTTTAAACAAAGTCAATGATGAAGCGCTTTCTTCTTAAATAAAGGAG 240
841 CAGCACTACTTTAAACAAAGTCAATGATGAAGCGCTTTCTTCTTAAATAAAGGAG 900
241 ATTCACTCTTAAGATTAATATGATGATGATGATGATGATGATGATGATGATGATGAT 300
901 ATTCACTCTTAAGATTAATATGATGATGATGATGATGATGATGATGATGATGATGAT 960
301 AGGAGAGCTGGAGAGGCAATGCTTAAGGAAAGAGGCGAGGCTTGAACCTCGAGCATC 360
961 AGGAGAGCTGGAGAGGCAATGCTTAAGGAAAGAGGCGAGGCTTGAACCTCGAGCATC 1020
361 CCATGAGCCGAGACAAAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
1021 CCATGAGCCGAGACAAAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
421 AGTTCTCCAAAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
1081 AGTTCTCCAAAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
481 AATCTTCCGTAATTCATTTTAAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
1141 AATCTTCCGTAATTCATTTTAAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
541 GGATAGAAAAAGCCCTGATACCTCAAGTATGATGATGATGATGATGATGATGATGATGAT 600
1201 GGATAGAAAAAGCCCTGATACCTCAAGTATGATGATGATGATGATGATGATGATGATGAT 1260
601 TAAAGAGCGAAAGCTTTCCCGGAGCTGGGGAAGGAGCAAGCTCTTCTTCATGCGCGAA 660
1261 TAAAGAGCGAAAGCTTTCCCGGAGCTGGGGAAGGAGCAAGCTCTTCTTCATGCGCGAA 1320
661 ATGGAACCTTAATTTCCCGTTCCCGCAACCAAGCCCGCGAGAGAGTCACTACAGAG 720

|||||
Db 1321 ATGGAATTTATTTCCCGTTCGCCCAACCAAGCCCGCCGAGAGAGTCTTCACAGAG 1380
OY 721 AGCCGCGAGATCAGCTTGGCCCAATCCGTGGCGTGGGGCCGCTCCCTTTATAGCCGA 780
Db 1381 AGCCGCGAGATCAGCTTGGCCCAATCCGTGGCGTGGGGCCGCTCCCTTTATAGCCGA 1440
OY 781 CTCGCCCGGAGCCGACCGGGTTC---GAGAGGTGGAGCTGGAGAGGCTGGGGCCAT 836
Db 1441 CTCGCCCGGAGCCGACCGGGTTCGGAGGAGAGGCTGGGGCTGGAGAGGCTGGGGCCAT 1500
OY 837 TTTTGTCTAACCTTAAGTGAAGAGGGCGTATGSCGCGCTGTTTGTCTCCCGCGCGCTG 896
Db 1501 TTTTGTCTAACCTTAAGTGAAGAGGGCGTATGSCGCGCTGTTTGTCTCCCGCGCGCTG 1560
OY 897 TTTTGTCTGAGCTTTCAGGGGGGAAAAAGCTCGGCGCTCGCGCGCTTCACAGCTTCAT 956
Db 1561 TTTTGTCTGAGCTTTCAGGGGGGAAAAAGCTCGGCGCTCGCGCGCTTCACAGCTTCAT 1620
OY 957 TCTAGAGCAAAACAAAAATGTCAGCTGTGCGCCCTTCGCGCGCGGGAGCTTCGCGC 1016
Db 1621 TCTAGAGCAAAACAAAAATGTCAGCTGTGCGCCCTTCGCGCGCGGGAGCTTCGCGC 1679
OY 1017 GCGTCCGCTCGCCCGCCGAGCCCGCCGCTGAGAGCCGCGGTGGCGCCGCGGCTTCGC 1076
Db 1680 GCGTCCGCTCGCCCGCCGAGCCCGCCGCTGAGAGCCGCGGTGGCGCCGCGGCTTCGC 1737
OY 1077 GAGGCGCACTACTGSCACCGGAGAGATT-GGGCTGTGTCAGCCGGGCTCTCTCGGGGC 1135
Db 1738 GAGGCGCACTACTGSCACCGGAGAGATTGGGCTGTGTCAGCCGGGCTCTCTCGGGGC 1797
OY 1136 GAGGCGGAGTTGAGGCGCTTTCAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1195
Db 1798 GAGGCGGAGTTGAGGCGCTTTCAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1855
OY 1196 GGGGCGATTCCTGAGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1255
Db 1856 GGGGCGATTCCTGAGAGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1915
OY 1256 TTTTCTGTTGGTGGGGGAGAGCGGATCGTGGCATCCGTCACCCCTCGCGCGGAGTGGG 1315
Db 1916 TTTTCTGTTGGTGGGGGAGAGCGGATCGTGGCATCCGTCACCCCTCGCGCGGAGTGGG 1975
OY 1316 GCGTGTGAGAGCCCAAACTGACTGAGTGGGAGTGGCTGCAAAATTGGCAGGAGAG 1375
Db 1976 GCGTGTGAGAGCCCAAACTGACTGAGTGGGAGTGGCTGCAAAATTGGCAGGAGAG 2035
OY 1376 TGAAGGACACTCCAAAGTGGGCCAAATGAATGGGAGTGAAGCGGGGGTGGCTGAGGC 1435
Db 2036 TGAAGGACACTCCAAAGTGGGCCAAATGAATGGGAGTGAAGCGGGGGTGGCTGAGGC 2095
OY 1436 GTTTCGTCGCTGGGCTCCGCTTCGCGTTCGCTTGTGCTTTTATGGTGTATTCAC 1495
Db 2096 GTTTCGTCGCTGGGCTCCGCTTCGCGTTCGCTTGTGCTTTTATGGTGTATTCAC 2155
OY 1496 TTTAGTTCCTGCTGAGATTTTGTGAGGTTTGTCTCTCCCAAGGATGATCTCGACC 1555
Db 2156 TTTAGTTCCTGCTGAGATTTTGTGAGGTTTGTCTCTCCCAAGGATGATCTCGACC 2215
OY 1556 AGTCCCTCAAGCGGGGTGGGAGACAGTCAATTTTGTGAGAGATGATTAACATTT 1615
Db 2216 AGTCCCTCAAGCGGGGTGGGAGACAGTCAATTTTGTGAGAGATGATTAACATTT 2275
OY 1616 AATGAATATTTATTAAGAAGATCTAATGACATTTGGAATTTGTTTCTTTAATGGTCA 1675
Db 2276 AATGAATATTTATTAAGAAGATCTAATGACATTTGGAATTTGTTTCTTTAATGGTCA 2335
OY 1676 TCGGTTTATGCGAGAGAGTGAAGTTTCTTTTGAAGAAATTAAGACCTTGGGATGACT 1735
Db 2336 TCGGTTTATGCGAGAGAGTGAAGTTTCTTTTGAAGAAATTAAGACCTTGGGATGACT 2395
OY 1736 TGAGCAGTAGATATTAACCCCAAGCTT 1765
|||||

Db 2396 TGAGCAGTAGATATTAACCCCAAGCTT 2425
RESULT 10
US-08-520-550A-1
; Sequence 1, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeneuve, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-9540
; TELEFAX: 617-861-6240
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-520-550A-1
Query Match 93.0%; Score 1640.8; DB 3; Length 2425;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1742; Conservative 0; Mismatches 17; Indels 11; Gaps 8;
OY 1 AGCTACGAGAGGCTGAGACACGAGATTCGCTGAAACCCCGGAGGAGAGCTTGCAGTG 60
Db 602 AGCTACGAGAGGCTGAGACACGAGATTCGCTGAAACCCCGGAGGAGAGCTTGCAGTG 720
OY 61 AGCCGAGATCAGCGCACCTAGACTCATTCCAGCTGGGGAGAAAGCAAGACTCCGCTCA 120
Db 721 AGCCGAGATCAGCGCACCTAGACTCATTCCAGCTGGGGAGAAAGCAAGACTCCGCTCA 780
OY 121 AAAAAAAAAATCGTTACATTTATGTGAGATTACTCCCTCTTTTACCTCATCAAGACA 180
Db 781 AAAAAAAAAATCGTTACATTTATGTGAGATTACTCCCTCTTTTACCTCATCAAGACA 840

QY	181	CAGCAGACTTTTAAAGCAAGCTCAATGATTTGGAAGCCCTTCTTCTTCTAATAAAGGAG	240
Db	841	CAGCAGCTACTTTTAAAGCAAGCTCAATGATTTGGAAGCCCTTCTTCTTCTAATAAAGGAG	900
QY	241	ATTTCAGTCTTAAAGTAAATATATATGATAGTATACATCTTGATTTAAAGCCATCCTCGTCA	300
Db	901	ATTTCAGTCTTAAAGTAAATATATATGATAGTATACATCTTGATTTAAAGCCATCCTCGTCA	960
QY	301	AGGAGAAGCTGAGGAAGGCAATTTCTTAAGGAAAAAGGCGCAGGTTGGAACCTGGACGCATC	360
Db	961	AGGAGAAGCTGAGGAAGGCAATTTCTTAAGGAAAAAGGCGCAGGTTGGAACCTGGACGCATC	1020
QY	361	CCATGAGAGCCGAGACAAGATTTGCTGTAGTCAGTCTCCTGGGAATCTATTTTTCAAA	420
Db	1021	CCATGAGAGCCGAGACAAGATTTGCTGTAGTCAGTCTCCTGGGAATCTATTTTTCAAA	1080
QY	421	AGTTCTCCAAAAATGTGATGATCAAAACTAGGAATTAAGTGTGTCTTAAAGCCCTA	480
Db	1081	AGTTCTCCAAAAATGTGATGATCAAAACTAGGAATTAAGTGTGTCTTAAAGCCCTA	1140
QY	481	AAATCTTCAGTGAATTCCTTTTAAAGGTAGCGAGGTGAACGCGCTGTGTGCGAGA	540
Db	1141	AAATCTTCAGTGAATTCCTTTTAAAGGTAGCGAGGTGAACGCGCTGTGTGCGAGA	1200
QY	541	GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAGGTGCGAAG	600
Db	1201	GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAGGTGCGAAG	1260
QY	601	TAAAGACGCAAAAGCTTTTCCCGGAGCTGGGGAAGGCAACGTCCTCTCATGGCCGAA	660
Db	1261	TAAAGACGCAAAAGCTTTTCCCGGAGCTGGGGAAGGCAACGTCCTCTCATGGCCGAA	1320
QY	661	ATGGAACCTTAAATTTCCCGTCCCGCCCAACCAAGCCGCGCGAGAGAGTACTACAG	720
Db	1321	ATGGAACCTTAAATTTCCCGTCCCGCCCAACCAAGCCGCGCGAGAGAGTACTACAG	1380
QY	721	AGCCGCGAGAGTCAAGCTTGGCCCAATCCGTGCGGTGGGCGCCGCTCCCTTATAAGCGA	780
Db	1381	AGCCGCGAGAGTCAAGCTTGGCCCAATCCGTGCGGTGGGCGCCGCTCCCTTATAAGCGA	1440
QY	781	CTCCGCGGAGGCGACACGGGTTGC --- GGAAGGTGGGCTGGGAAGGAGGTGGGCCAT	836
Db	1441	CTCCGCGGAGGCGACACGGGTTGC --- GGAAGGTGGGCTGGGAAGGAGGTGGGCCAT	1500
QY	837	TTTTTGTCTAACCTTAAGAGAGGCGTAGGCGCGCTGCTTTTGTCTCCCGCGCGCTG	896
Db	1501	TTTTTGTCTAACCTTAAGAGAGGCGTAGGCGCGCTGCTTTTGTCTCCCGCGCGCTG	1560
QY	897	TTTTTTCGCTGACTTTCAGCGGGGCGAAAAAGCTTGCGCTCGCGCTTCCACGCTTCAT	956
Db	1561	TTTTTTCGCTGACTTTCAGCGGGGCGAAAAAGCTTGCGCTCGCGCTTCCACGCTTCAT	1620
QY	957	TCTAGACAACAAAAAATTCAGTGTGCGCGCGTCCGCTCCGCGGAGCGTCCGCGC	1016
Db	1621	TCTAGACAACAAAAAATTCAGTGTGCGCGCGTCCGCTCCGCGGAGCGTCCGCGC	1676
QY	1017	GGGTGCGCTCCAGCGCCCGGAAACCCCGCTGAGGCGCGGCTGGCGCGGGGCTTCTC	1076
Db	1680	GGGTGCGCTCCAGCGCCCGGAAACCCCGCTGAGGCGCGGCTGGCGCGGGGCTTCTC	1736
QY	1077	GGAGAGCACTACAGCACGCGCGAAAGATT -GGCTGTGTACGCGCGGGGTCTGTGGGGG	1136
Db	1738	GGAGAGCACTACAGCACGCGCGAAAGATT -GGCTGTGTACGCGCGGGGTCTGTGGGGG	1196
QY	1136	GAGGCGCAGGTTTCAAGGCTTTTCAAGCGCGCAGAGAAGAGAAAGCAAGCAGATCCCGCGC	1195
Db	1798	GAGGCGCAGGTTTCA -CGGTTTCAAGCGCGCAGAGAAGAGAAAGCAAGCAGATCCCGCGC	1855
QY	1196	GCGCGCATTTCCCTGAGCTGTGGGAGCTGCACCCAGAGCTCGGCTACACATGCACTTGC	1255
Db	1856	GCGCGCATTTCCCTGAGCTGTGGGAGCTGCACCCAGAGACTCGGCTACACATGCACTTGC	1915

Oy	1256	TTTTCTGTGGTGGGGGAACGGCCAMTCGGGCATCCGTCAACCCCTGGCCGACAGTGG	1315
Db	1916	TTTTCTGTGGTGGGGGGAACGCCGATCGTGGCATCCGTCAACCCCTGGCCGACAGTGG	1975
Oy	1316	GGCTTGTGAACCCCAAACTGACTGACTGGGCACTGTGCTGCAAAATTGGCAGAGACG	1375
Db	1976	GGCTTGTGAACCCCAAACTGACTGACTGGGCACTGTGCTGCAAAATTGGCAGAGACG	2035
Oy	1376	TGAAGGACCTCCAAAGTGGGGCAAAATGAATGGGAGAGACCGGGGTGGCTGGAGCC	1435
Db	2036	TGAAGGACCTCCAAAGTGGGGCAAAATGAATGGGAGAGACCGGGGTGGCTGGAGCC	2095
Oy	1436	GTTCCGTGCGGTGTTTCCCGCTTCCGCTTTTGTGGCTTTAATGTTGATTAAC	1495
Db	2096	GTTCCGTGCGGTGTTTCCCGCTTCCGCTTTTGTGGCTTTAATGTTGATTAAC	2155
Oy	1496	TTATCTCTGCTCGCAGATTTTGTGAGTTTTGCTCTGCCAAGTAATCTCGACC	1555
Db	2156	TTATCTCTGCTCGCAGATTTTGTGAGTTTTGCTCTGCCAAGTAATCTCGACC	2215
Oy	1556	AGTCCCTCAACGGGGGTGGGGAACAGTCATTTTTTTTGAAGATCATTTAAACATT	1615
Db	2216	AGTCCCTCAACGGGGGTGGGGAACAGTCATTTTTTTTGAAGATCATTTAAACATT	2275
Oy	1616	AATGAATATTTAATTAGAAAGTCTAAATGAACATTGGAAATGTGTTCTCTTAATGTCA	1675
Db	2276	AATGAATATTTAATTAGAAAGTCTAAATGAACATTGGAAATGTGTTCTCTTAATGTCA	2335
Oy	1676	TGCGTTTATGCAAGAGGTGTGAAGTTCCTTTTTTGAATAATAGACCTTGCGATGACT	1735
Db	2336	TGCGTTTATGCAAGAGGTGTGAAGTTCCTTTTTTGAATAATAGACCTTGCGATGACT	2395
Oy	1736	TGAGCAGTAGATATTAACCCCAAGCTT	1765
Db	2396	TGAGCAGTAGATATTAACCCCAAGCTT	2425

RESULT 11
 US-08-714-482-2
 : Sequence 2, Application US/08714482
 : Patent No. 5972605
 :
 : GENERAL INFORMATION:
 : APPLICANT: Villeponteau, Bryant
 : APPLICANT: Harley, Calvin
 : TITLE OF INVENTION: Assays for Regulators of Mammalian
 : TITLE OF INVENTION: Telomerase Expression
 : NUMBER OF SEQUENCES: 2
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Townsend and Townsend and Crew LLP
 : STREET: Two Embarcadero Center, Eighth Floor
 : CITY: San Francisco
 : STATE: California
 :
 : COUNTRY: USA
 :
 : ZIP: 94111-3834
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/714,482
 : FILING DATE: 16-SEP-1996
 : CLASSIFICATION: 435
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/521,634
 : FILING DATE: 31-AUG-1995
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/482,115
 : FILING DATE: 07-JUN-1995
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/472,802
 : FILING DATE: 07-JUN-1995
 :
 : PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00860US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..981
OTHER INFORMATION: /note="PstI fragment containing hTR
OTHER INFORMATION: sequence"
US-08-714-482-2

Query Match 54.8%; Score 967.4; DB 2; Length 981;
Best Local Similarity 99.8%; Pred. No. 1.7e-271;
Matches 979; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
DB 534 CTGCAGAGATAGAAAAAGGCCCTTGATACCTCAAGTTAGTTACCTTTAAGAGG 593
1 CTGCAGAGATAGAAAAAGGCCCTTGATACCTCAAGTTAGTTACCTTTAAGAGG 60
DB 594 TCGGAGTAAAGACGCAACCTTTCCGAGCGTGGGAGGAGGCAAGTCTTCATG 653
61 TCGGAGTAAAGACGCAACCTTTCCGAGCGTGGGAGGAGGCAAGTCTTCATG 120
DB 654 GCCGGAATGGAATTTATTTCCCGTTCCCGCAACGAGCCCGCGAGAGAGTACTC 713
121 GCCGGAATGGAATTTATTTCCCGTTCCCGCAACGAGCCCGCGAGAGAGTACTC 180
DB 714 TCACGAGACCGGAGAGTACGTTGCCAATCCGTGGCGGCGGCTCCCTTTAT 773
181 TCACGAGACCGGAGAGTACGTTGCCAATCCGTGGCGGCGGCTCCCTTTAT 240
DB 774 AAGCCGACTGCGCGGACGCGACCGGCTTGGCGAGGCTGGAGGAGGAGTGGC 833
241 AAGCCGACTGCGCGGACGCGACCGGCTTGGCGAGGCTGGAGGAGGAGTGGC 300
DB 834 CATTTTGTCTAACCCTTAAGAGAGGCGTAGGCGCGCTTTTGTCTCCCGCGC 893
301 CATTTTGTCTAACCCTTAAGAGAGGCGTAGGCGCGCTTTTGTCTCCCGCGC 360
DB 894 CTGTTTCTGCTGACTTTCAGCGGCGGAAAGCGTGGCGCGCTCCCGCTCCACCGT 953
361 CTGTTTCTGCTGACTTTCAGCGGCGGAAAGCGTGGCGCGCTCCCGCTCCACCGT 420
DB 954 CATTTAGAGCAAAATAATGTAGCTGTGGCCGCTTCCCGCTCCCGGAGACTGC 1013
421 CATTTAGAGCAAAATAATGTAGCTGTGGCCGCTTCCCGCTCCCGGAGACTGC 480
DB 1014 GCGGGGTGCGCGCCGAGCGCCGCAACCCGCTGAGAGCGCGCGTCCCGGCGCTTC 1073
481 GCGGGGTGCGCGCCGAGCGCCGCAACCCGCTGAGAGCGCGCGTCCCGGCGCTTC 540
DB 1074 TCCGAGGACCTTACTGCGACCGCAAGAGTT-GGCTCTGTAGCGCGGAGTCTCGGG 1132
541 TCCGAGGACCTTACTGCGACCGCAAGAGTTGGGCTCTGTAGCGCGGAGTCTCGGG 600
DB 1133 GCGGAGGCGGAGCTTACGCGCTTTAGGCGCGAGAGAGAGAGAGTCCCGCG 1192
601 GCGGAGGCGGAGCTTACGCGCTTTAGGCGCGAGAGAGAGAGAGTCCCGCG 660

DB 1193 CGCGGCGCATTCCTGACCTGAGAGTGCACCCAGAGACTGCGCTACACATGCACTT 1252
661 CGCGGCGCATTCCTGACCTGAGAGTGCACCCAGAGAGTGCACATGCACTT 720
DB 1253 CGCTTCTGTTGTGGGGGAAGCCGATGCGCATCCGTCACCCCTGCGCGAGT 1312
721 CGCTTCTGTTGTGGGGGAAGCCGATGCGCATCCGTCACCCCTGCGCGAGT 780
DB 1313 GGGGCTTGTGAACCCCAACCTGACTGAGTGGCCAGTGTGCTGAATTTGGCAGAG 1372
781 GGGGCTTGTGAACCCCAACCTGACTGAGTGGCCAGTGTGCTGAATTTGGCAGAG 840
DB 1373 ACGTGAAGCAGCTCCAAAGTGGCCAAATGAATGGGAGAGAGCGGGTGGCTGGA 1432
841 ACGTGAAGCAGCTCCAAAGTGGCCAAATGAATGGGAGAGAGCGGGTGGCTGGA 900
DB 1433 GCCGTTCTGCTGGGTTCTCCGCTTCCGCTTTTGTGCTTTATGTTGATTTAC 1492
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DB 1493 AACTTAGTTCTGCTGTCAG 1513
961 AACTTAGTTCTGCTGTCAG 981

RESUL# 12
US-08-710-249-5
Sequence 5, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: misc_RNA
 LOCATION: 267..715
 OTHER INFORMATION: /product="hnr"
 OTHER INFORMATION: /note="hnr transcript serves as
 OTHER INFORMATION: template in the telomerase
 OTHER INFORMATION: ribonucleoprotein"
 US-08-710-249-5

Query Match 54.8%; Score 966.4; DB 2; Length 981;
 Best Local Similarity 99.7%; Pred. No. 3,4e-271;
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 534 CTGCAGAGATTAAGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 593
 DB 1 CTGCAGAGATTAAGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 60
 QY 594 TCGGAAGTAAAGACGCAAGCCCTTCCGAGAGTGGGAAGGCGCAAGTCTCTCATG 653
 DB 61 TCGGAAGTAAAGACGCAAGCCCTTCCGAGAGTGGGAAGGCGCAAGTCTCTCATG 120
 QY 654 GCGGGAATGGAAGCTTTAATTTCCCGTCCCAACACAGCCCGCGAGAGAGTCACTC 713
 DB 121 GCGGGAATGGAAGCTTTAATTTCCCGTCCCGTCCCAACACAGCCCGCGAGAGTCACTC 180
 QY 714 TCACGAGAGCGCGAGAGTCACTTGGCCATCCGTGCGGTGGCGCGCTCTTTAT 773
 DB 181 TCACGAGAGCGCGAGAGTCACTTGGCCATCCGTGCGGTGGCGCGCTCTTTAT 240
 QY 774 AACCCGACTGCGCGAGAGCGCAAGGCTTGGAGAGGCTGGCGTGGAGAGGCTGGG 833
 DB 241 AACCCGACTGCGCGAGAGCGCAAGGCTTGGAGAGGCTGGCGTGGAGAGGCTGGG 300
 QY 834 CATTTTGTCTAACCCTTAAGAGAGGCGTGGCGCGCTCTTTGCTCCCGCGCG 893
 DB 301 CATTTTGTCTAACCCTTAAGAGAGGCGTGGCGCGCTCTTTGCTCCCGCGCG 360
 QY 894 CTGTTTTCCTGCTGACTTTCACGCGGCGGAAAGCTTGGCGCTTCCCGCTTCCACCGTT 933
 DB 361 CTGTTTTCCTGCTGACTTTCACGCGGCGGAAAGCTTGGCGCTTCCCGCTTCCACCGTT 420
 QY 954 CATTTAGACCAAAACAAAATGTCAGCTGTGGCGCTTGGCGCTTCCCGCTTCCCGGAGCTGCG 1013
 DB 421 CATTTAGACCAAAACAAAATGTCAGCTGTGGCGCTTGGCGCTTCCCGCTTCCCGGAGCTGCG 480
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 QY 1074 TCGGAGAGCACTACTGCGCAACCGCGGAAGTT-GGCTCTGTCAAGCGCGGGTCTCTCGGG 1132
 DB 541 TCGGAGAGCACTACTGCGCAACCGCGGAAGTTGGGCTGTGTCAAGCGCGGGTCTCTCGGG 600
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 QY 1313 GCGGAGCTTGAAGCCCAACCTGACTGACTGGCCAGTGTCTGCAATTTGGCAGAG 1372
 DB 781 GCGGAGCTTGAAGCCCAACCTGACTGACTGGCCAGTGTCTGCAATTTGGCAGAG 840
 QY 1373 ACGTGAAGGACCTCCAAAGTCGCGCAAAATGATGGGAGTGAAGCGCGGGTGTGCTTGA 1432
 DB 841 ACGTGAAGGACCTCCAAAGTCGCGCAAAATGATGGGAGTGAAGCGCGGGTGTGCTTGA 900

QY 1433 GCGGTCCTGCGCGTGGGTCTCCCGCTTTCGCGCTTTTGTGCTTTATGTTATATAC 1492
 DB 901 GCGGTCCTGCGCGTGGGTCTCCCGCTTTCGCGCTTTTGTGCTTTATGTTATATAC 960
 QY 1493 AACTAGTCTCTGCTGCGAG 1513
 DB 961 AACTAGTCTCTGCTGCGAG 981

RESULT 13

US-09-220-157A-5
 Sequence 5; Application US/09220157A
 Patent No. 6300110

GENERAL INFORMATION:
 APPLICANT: Villeponteau, Bryant
 APPLICANT: Feng, Junli
 APPLICANT: Andrews, William H.
 APPLICANT: Adams, Robert R.
 TITLE OF INVENTION: Methods and Reagents for Regulating
 TITLE OF INVENTION: Telomere Length and Telomerase Activity
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/220,157A
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/710,249
 FILING DATE: 13-SEP-1996
 APPLICATION NUMBER: US 08/583,808
 FILING DATE: 05-JAN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/003,492
 FILING DATE: 08-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 32,944
 REFERENCE/DOCKET NUMBER: 015389-001220US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 981 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:

NAME/KEY: misc_RNA
 LOCATION: 267..715
 OTHER INFORMATION: /product="hnr"
 OTHER INFORMATION: /note="hnr transcript serves as
 OTHER INFORMATION: template in the telomerase
 OTHER INFORMATION: ribonucleoprotein"
 US-09-220-157A-5

Query Match 54.8%; Score 966.4; DB 4; Length 981;
 Best Local Similarity 99.7%; Pred. No. 3,4e-271;
 Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY	534	CTGCAGAGAAATGAAAAAAGGCCCTCGATATACGTCACAGATTAGTTTACCTTTAAAGAG	593
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Db	61	TCGGAAGTAAAGACGCCAAGCCTTTCCGGACGTGGCGAAGGGCAACGTCCTTCTCATG	120
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Db	121	GCCGGAATATGAACTTAAATTTCCGTTCCCTCCACACAGCCGCGCGAGAGATGATC	180
OY	714	TCACAGAGACCCGCGAGAGTCAGCTTGGCCAAATCCGTCCGTCCGCGCCTCTTAT	240
Db	181	TCACAGAGACCCGCGAGAGTCAGCTTGGCCAAATCCGTCCGCGCCTCTCTTAT	240
OY	774	AAGCCGACTCCGCGCGACCGGGTTCCGAGAGGTGGAGGTGGAGAGGGTGGG	833
Db	241	AAGCCGACTCCGCGCGACCGGGTTCCGAGAGGTGGAGGTGGAGAGGGTGGG	300
OY	834	CATTTTGTGTATACCCCTTACCTGAGAAAGGGGATAGCGCCGTGCTTGTCTCCCGCG	893
Db	301	CATTTTGTGTATACCCCTTACCTGAGAAAGGGGATAGCGCCGTGCTTGTCTCCCGCG	360
OY	894	CGTGTTCCTGCGTACCTTACGAGGGGGGAAAGCCTCGCCCTCGCCCTTCCACCGT	953
Db	361	CGTGTTCCTGCGTACCTTACGAGGGGGGAAAGCCTCGCCCTCGCCCTTCCACCGT	420
OY	954	CATTCTAGAGCAACAAAAATGTCTACGTGCTGGCCGTTCCGCCCTCCCGGGAGCTGC	1011
Db	421	CATTCTAGAGCAACAAAAATGTCTACGTGCTGGCCGTTCCGCCCTCCCGGGAGCTGC	480
OY	1014	GCGCGGTCGCTGGCCGACGCCCCCGAACCCTGCGAGAGGCGCGGTCGCGCGGGCTTC	107
Db	481	GCGCGGTCGCTGGCCGACGCCCCCGAACCCTGCGAGAGGCGCGGTCGCGCGGGCTTC	540
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Db	541	TCGCGAGGCACTTACTGCGACCGCGGAAGATT--GGCTGTGTCAAGCCGCGGGTCTTCGG	600
OY	1133	GCGCGAGGCGAGGTTCAAGGCTTTCAGGCGCGAGAGAGAGAAAGGAGCGAGTCCCGG	119
Db	601	GCGCGAGGCGAGGTTCAAGGCTTTCAGGCGCGAGAGAGAGAAAGGAGCGAGTCCCGG	660
OY	1193	GCGGCGGCGATTCCTGAGCTGTGGGACGTGACCCACGAGCATCGGCTACACATGCAATT	125
Db	661	GCGGCGGCGATTCCTGAGCTGTGGGACGTGACCCAGCATCGGCTACACATGCAATT	720
OY	1253	GCGTTTCCTGTTGGGGGGGGAACGCGATGCGGCGATCGATCGACCCCTCGCGGCACT	131
Db	721	GCGTTTCCTGTTGGGGGGGGAACGCGATGCGGCGATCGATCGACCCCTCGCGGCACT	780
OY	1313	GGGGCGTTGTGAACCCCAACCTGACTGTGGCCAGTGTCTGCAATTTGGCAGAG	137
Db	781	GGGGCGTTGTGAACCCCAACCTGACTGTGGCCAGTGTCTGCAATTTGGCAGAG	840
OY	1373	ACGTGAAGGCACTTCCAAAGTCGCGCAAAATGAATGGGCACTAGCGCGGGTTCCTGGA	143
Db	841	ACGTGAAGGCACTTCCAAAGTCGCGCAAAATGAATGGGCACTAGCGCGGGTTCCTGGA	900
OY	1433	GCGGTCCTGCGTGGGTTCTCCGCTTTCGCGCTTTTGTGTGCTTTATGGTTGATTAC	1491
Db	901	GCGGTCCTGCGTGGGTTCTCCGCTTTCGCGCTTTTGTGTGCTTTATGGTTGATTAC	960
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RESULT 14
US-08-770-565-1
; Sequence 1, Application US/08770565
; Patent No. 5846723

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1: GENERAL INFORMATION:
2: APPLICANT: Kim, Nam Woo
3: APPLICANT: Wu, Fred
4: APPLICANT: Kealey, James T.
5: APPLICANT: Pruzan, Ronald
6: APPLICANT: Weinlich, Scott L.
7: TITLE OF INVENTION: Methods for Detecting the RNA Component of
8: TITLE OF INVENTION: Telomerase
9: NUMBER OF SEQUENCES: 26
10: CORRESPONDENCE ADDRESS:
11: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
12: STREET: Two Embarcadero Center, 8th Floor
13: CITY: San Francisco
14: STATE: California
15: COUNTRY: USA
16: ZIP: 94111-3834
17: COMPUTER READABLE FORM:
18: MEDIUM TYPE: Floppy disk
19: COMPUTER: IBM PC compatible
20: OPERATING SYSTEM: PC-DOS/MS-DOS
21: SOFTWARE: Patent In Release #1.0, Version #1.30
22: CURRENT APPLICATION DATA:
23: APPLICATION NUMBER: US/08/770.565
24: FILING DATE: 20-DEC-1996
25: CLASSIFICATION: 435
26: ATTORNEY/AGENT INFORMATION:
27: NAME: Storella, John R.
28: REGISTRATION NUMBER: 32,944
29: REFERENCE/DOCKET NUMBER: 015389-002300US
30: TELECOMMUNICATION INFORMATION:
31: TELEPHONE: 415-576-0200
32: TELEFAX: 415-576-0300
33: INFORMATION FOR SEQ ID NO: 1:
34: SEQUENCE CHARACTERISTICS:
35: LENGTH: 981 base pairs
36: TYPE: nucleic acid
37: STRANDEDNESS: double
38: TOPOLOGY: linear
39: MOLECULE TYPE: DNA (genomic)
40: US-08-770-565-1

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Query Match	54.7%	Score 965.8	DB 2	Length 981
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QY 534	CTGCAGAGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAAAG	593		
Db 1	CTGCAGAGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAAAG	60		
QY 594	TTCGAAAGTAAGAACCCAAAGCCTTTCCCGGAGCTCCGGAAGGGCAAGCTCTCTCATG	653		
Db 61	TTCGAAAGTAAGAACCCAAAGCCTTTCCCGGAGCTCCGGAAGGGCAAGCTCTCTCATG	120		
QY 654	GCCGGAATATGAACTTTATTTCCCGTTCCCAACAGCCCGCCGAGAGATGACATC	713		
Db 121	GCCGGAATATGAACTTTATTTCCCGTTCCCAACAGCCCGCCGAGAGATGACATC	180		
QY 714	TCAGAGAGAGCCGCGAGATCACTTGGCCAAATCGCTGGCTGGCGCCCTCCCTTAT	773		
Db 181	TCAGAGAGAGCCGCGAGATCACTTGGCCAAATCGCTGGCTGGCGCCCTCCCTTAT	240		
QY 774	AAGCGATCTCCCGCGCAGCGACCGGGTTGGGAGGGCTGGGGCAAGGGGTGTGGC	833		
Db 241	AAGCGATCTCCCGCGCGAGCGACCGGGTTGGGAGGGGTGGGGCAAGGGGTGTGGC	300		
QY 834	CATTTTGTCTAAACCTCACTGAGAAAGGGCTAGGCGCCGTTTGTCTCCCGCCG	893		
Db 301	CATTTTGTCTAAACCTCACTGAGAAAGGGCTAGGCGCCGTTTGTCTCCCGCGG	360		
QY 894	CTGTTTTCCTGCGTACCTTACAGGGGGGGAAGAGCTTCGGCTTCGCCCTTCCACCGTT	953		
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OY 954 CATCTAGAGCAAAACAAAATGTGAGCTGTGGCCCGTCCCGCCCGGAGACTGC 1013
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DB 481 GCGGGGTGCGCCCGCCAGCCCGGAAACCCCGCTGAGAGCCCGGTGCGCCGCTTC 540
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DB 781 GGGGCGTTGTGAACCCCGCAACCTGACTGACTGTGGCCAGTGTGTGCAAAATTGGCAGAG 840
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OY 1433 GCGGTTCCGTGTGTGGGGGTTTCCCGTCTTCCGCTTTTGTGCTTTTATGATTAATAC 1492
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DB 901 GCGGTTCCGTGTGTGGGGGTTTCCCGTCTTCCGCTTTTGTGCTTTTATGATTAATAC 960
OY 1493 AACTAGTTCCTGCTCTGCAG 1513
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DB 961 AACTAGTTCCTGCTCTGCAG 981

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RESULT 15
US-08-833-377-1
: Sequence 1, Application US/08833377
: Patent No. 5968506
: GENERAL INFORMATION:
: APPLICANT: Weinlich, Scott L.
: APPLICANT: Atkinson III, Edward M.
: APPLICANT: Lichtenstein, Serge P.
: APPLICANT: Vasserot, Alain P.
: APPLICANT: Pruzan, Ronald A.
: APPLICANT: Kealey, James T.
: TITLE OF INVENTION: Purified Telomerase
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/833,377
: FILING DATE: 04-APR-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/510,736
: FILING DATE: 04-AUG-1995

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: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: REFERENCE/DOCKET NUMBER: 015389-001110US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 981 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY:
: LOCATION: 1..981
: OTHER INFORMATION:
: OTHER INFORMATION: Sautiral-HindIII fragment of clone 28-1"
US-08-833-377-1

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Query Match          54.7%: Score 965.8: DB 2: Length 981:
Best Local Similarity 99.7%: Pred. No. 5e-271:
Matches 978: Conservative 0: Mismatches 2: Indels 1: Gaps 1:

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OY 534 CTGCAGAGGATGAAAAAGGCCCTGTGATACCTGATTAATTCACCTTTAAAGAGG 593
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DB 1 CTGCAGAGGATGAAAAAGGCCCTGTGATACCTGATTAATTCACCTTTAAAGAGG 60
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OY 954 CATCTAGAGCAAAACAAAATGTGAGCTGTGGCCCGTCCCGCCCGGAGACTGC 1013
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OY 1193 GCGGCGCGGATTCCTGAGCTGTGGAGAGTGCACCCAGAGACTGCGCTCAGACATGACATT 1252
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QY 1433 GCCGTTCCCTGGGTGCTCCCGTCTCCGCTTTTGTGCTTATGCTGATTTAC 1492
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

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Searched: 356696 seqs, 198428768 residues

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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1719.6	97.4	2426	10	US-09-057-351-3
2	883.4	50.1	4118	10	US-09-068-821-17
3	881.6	49.9	962	10	US-09-018-125-1
4	881.6	49.9	962	10	US-09-068-821-16
5	841.6	47.7	975	10	US-09-068-821-20
6	835.4	47.3	4118	10	US-09-068-821-18
7	835.2	47.3	975	10	US-09-068-821-21
8	830.4	47.0	975	10	US-09-068-821-19
9	546.4	31.0	560	10	US-09-057-351-1
10	101.8	5.8	180216	10	US-09-835-232-6
11	101.2	5.7	32193	10	US-09-764-877-2623
12	101.2	5.7	684973	10	US-09-263-959-1
13	99.6	5.6	302250	10	US-09-962-832-154
14	99.2	5.6	9914	10	US-09-764-847-1558
15	99	5.6	31994	9	US-09-764-904-71
16	99	5.6	31994	9	US-09-764-860-599
17	98.6	5.6	28897	10	US-09-764-877-3897
18	98	5.6	289	10	US-09-764-877-2732
19	97.6	5.5	2756	10	US-09-764-853-898

c 20	97.4	5.5	27148	10	US-09-764-860-1046	Sequence 1046, Ap
21	97	5.5	10885	10	US-09-764-877-3843	Sequence 3843, Ap
22	96.4	5.5	30625	10	US-09-927-091-5	Sequence 5, Appl1
c 23	96.4	5.5	32187	10	US-09-764-847-1550	Sequence 1550, Ap
c 24	96.4	5.5	32193	10	US-09-764-847-1549	Sequence 1549, Ap
c 25	96.4	5.5	145831	10	US-09-969-708-79	Sequence 79, Appl
c 26	96.4	5.5	145831	10	US-09-954-456-2116	Sequence 2116, Ap
c 27	96	5.4	303	10	US-09-764-870-604	Sequence 604, App
c 28	96	5.4	1115	9	US-09-981-353-126	Sequence 126, App
c 29	96	5.4	1545	10	US-09-764-877-3172	Sequence 3172, Ap
c 30	96	5.4	10378	10	US-09-764-847-1616	Sequence 1616, Ap
c 31	96	5.4	10472	10	US-09-764-847-1615	Sequence 1615, Ap
c 32	96	5.4	17752	10	US-09-748-127-3	Sequence 3, Appl1
c 33	96	5.4	32185	10	US-09-764-877-3171	Sequence 3171, Ap
c 34	96	5.4	32193	9	US-09-764-868-1508	Sequence 1508, Ap
c 35	96	5.4	53542	10	US-09-801-574-61	Sequence 61, Appl
c 36	96	5.4	98865	10	US-09-770-6894-3	Sequence 3, Appl1
c 37	95.8	5.4	2240	10	US-09-814-292-1	Sequence 7043, Ap
c 38	95.6	5.4	423	10	US-09-867-701-7043	Sequence 3, Appl1
c 39	95.4	5.4	36159	12	US-10-135-687-3	Sequence 1963, Ap
c 40	95	5.4	32169	10	US-09-764-847-1963	Sequence 338, App
c 41	95	5.4	32190	10	US-09-764-887-338	Sequence 389, App
c 42	94.8	5.4	142	10	US-09-764-877-3289	Sequence 2040, Ap
c 43	94.8	5.4	4071	10	US-09-764-869-2040	Sequence 611, App
c 44	94.8	5.4	32195	10	US-09-764-870-611	Sequence 617, App
c 45	94.8	5.4	32195	10	US-09-764-870-617	

ALIGNMENTS

RESULT 1
US-09-057-351-3
Sequence 3, Application US/09057351
Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Valleponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/057,351
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-057-351-3

Query Match 97.4%; Score 1719.6; DB 10; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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QY 1 ACCTGCTGAGGCGGTGAGACAGGAAATCGCTTGAACCCGGGAGGAGAGAGTTGACAGT 60
DB 662 ACCTGCTGAGGCGGTGAGACAGGAAATCGCTTGAACCCGGGAGGAGAGTTGACAGT 720
QY 61 AGCCGAGATCAGCCGACTAGACTCCATCCAGCGCTGGGCGAAGAGCAAGATCCGCTCTCA 120
DB 721 ACCCGAGATCAGCCGACTAGACTCCATCCAGCGCTGGGCGAAGAGCAAGATCCGCTCTCA 780
QY 121 AAAAAAAAAATCGTTACATTTATGATGATTAATCTCCCTCTTTTACCTCATCAAGACA 180
DB 781 AAAAAAAAAATCGTTACATTTATGATGATTAATCTCCCTCTTTTACCTCATCAAGACA 840
QY 181 CAGCACTCTTTAAGCAAGTCATGATGAAAGCGCTTTCTTCTTCTTCTTCTTCTTCTTCTT 240
DB 841 CAGCACTCTTTAAGCAAGTCATGATGAAAGCGCTTTCTTCTTCTTCTTCTTCTTCTTCTT 900
QY 241 ATTGAGTCTTAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 901 ATTGAGTCTTAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 301 AGGAAAGCTGGAAGAGCATCTTAAGGAAAAAGGGGCGAGGTTGGAAGTGGAGCGATC 360
DB 961 AGGAAAGCTGGAAGAGCATCTTAAGGAAAAAGGGGCGAGGTTGGAAGTGGAGCGATC 420
QY 361 CCAGTGAAGCGGAGAGAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 420
DB 1021 CCAGTGAAGCGGAGAGAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 421 AGTCTCCAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 1081 AGTCTCCAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 481 AATGCTCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 1141 AATGCTCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 541 GGATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTAAAGAAAGTGGGAAG 600
DB 1201 GGATGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTCACTTAAAGAAAGTGGGAAG 1260
QY 601 TAAAGAGCAAAAGCTTTCCGCGAGCTGGGAGGGAAGGCAACGTCCTTCTCATGCGGAAA 660
DB 1261 TAAAGAGCAAAAGCTTTCCGCGAGCTGGGAGGGAAGGCAACGTCCTTCTCATGCGGAAA 1320
QY 661 ATGCAACTTTAATTTCCGCTTCCCGCCCAACGAGCCCGCCGAGAGAGTCTACAGAG 720
DB 1321 ATGCAACTTTAATTTCCGCTTCCCGCCCAACGAGCCCGCCGAGAGAGTCTACAGAG 1380
QY 721 AGCCGAGAGATCAGCTTGGCCAAATCGTGCGTGGGCGGCGCTTCTTATAAGCCGA 780
DB 1381 AGCCGAGAGATCAGCTTGGCCAAATCGTGCGTGGGCGGCGCTTCTTATAAGCCGA 1440
QY 781 CTCGCGCGGCAAGCGACCGGCTTGGGAGGGTGGGCTGGGAGGGGTTGGTGGCCATTTT 840
DB 1441 CTCGCGCGGCAAGCGACCGGCTTGGGAGGGTGGGCTGGGAGGGGTTGGTGGCCATTTT 1500
QY 841 TGTCTAACCTTAACAGAGGAAGGGGTAGGCGCGCTTTTGTCTCCCGCGCGCTGTTT 900
DB 1501 TGTCTAACCTTAACAGAGGAAGGGGTAGGCGCGCTTTTGTCTCCCGCGCGCTGTTT 1560
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QY 901 TCTCGCTGACTTTACGCGGGGGAAGACCTTGGCTTGGCTTCCACCTTCACTTCTTA 960
DB 1561 TCTCGCTGACTTTACGCGGGGGAAGACCTTGGCTTGGCTTCCACCTTCACTTCTTA 1620
QY 961 GAGCAAAACAAAAATGTACAGCTGCTGGCCGTTGCGCCCTCCGCGGAGCTGCGCGGGT 1020
DB 1621 GAGCAAAACAAAAATGTACAGCTGCTGGCCGTTGCGCCCTCCGCGGAGCTGCGCGGGT 1680
QY 1021 GCGCTGCGCCAGCGCCGGAACCCCGCTGGAGCGCGGCTGGCGCCCGGAGCTTCCGAG 1080
DB 1681 GCGCTGCGCCAGCGCCGGAACCCCGCTGGAGCGCGGCTGGCGCCCGGAGCTTCCGAG 1740
QY 1081 GCACCTACTGCGCACCGCGCAAGAGTT-GGCTCTGTACAGCGCGGGGCTCTCGCGGGCA 1139
DB 1741 GCACCTACTGCGCACCGCGCAAGAGTTGAGGCTGTACAGCGCGGGGCTCTCGCGGGCA 1800
QY 1140 GCGAGGTTCAAGGCTTTTACGCGCGGAGAGAGAGAACGAGAGGATCCCGCGCGGCG 1199
DB 1801 GCGAGGTTCAAGGCTTTTACGCGCGGAGAGAGAGAACGAGAGGATCCCGCGCGGCG 1860
QY 1200 CGATTCCCTGAGCTGTGGAGGTGCACCCAGGACTCGGCTCACAATGCAATGCACTTGGCTTTC 1259
DB 1861 CGATTCCCTGAGCTGTGGAGGTGCACCCAGGACTCGGCTCACAATGCAATGCACTTGGCTTTC 1920
QY 1260 CTGTTGGTGGGGGGAACCGCATGCTGCGCATCCGTCACCCCTCGCGCGGAGTGGGCT 1319
DB 1921 CTGTTGGTGGGGGGAACCGCATGCTGCGCATCCGTCACCCCTCGCGCGGAGTGGGCT 1980
QY 1320 TGTGAACCCCAACCTTACAGTACGAGTGGGCGAGTGGTGGCAATTTGGGAGAGAGTGA 1379
DB 1981 TGTGAACCCCAACCTTACAGTACGAGTGGGCGAGTGGTGGCAATTTGGGAGAGAGTGA 2040
QY 1380 GGCACCTCCAAAGTGCGCCAAATGATGAGGAGTGGAGTGGGCTGGGAGCGCTTC 1439
DB 2041 GGCACCTCCAAAGTGCGCCAAATGATGAGGAGTGGAGTGGGCTGGGAGCGCTTC 2100
QY 1440 CTGCGTGGGTTCTCCCGCTTCCGCTTGTGTTGCTTGTGTTGTTGTTGTTGTTGTTG 1499
DB 2101 CTGCGTGGGTTCTCCCGCTTCCGCTTGTGTTGCTTGTGTTGTTGTTGTTGTTGTTG 2160
QY 1500 TTCTGCTCTGACATTTTGTGAGGTTTGTGCTTCCCAAGTAGATCTGACCAATC 1559
DB 2161 TTCTGCTCTGACATTTTGTGAGGTTTGTGCTTCCCAAGTAGATCTGACCAATC 2220
QY 1560 CCTTCAAGGGGCTGGGAGAGAGTCAATTTTTTTTGTGAGATCATTTAATTAATG 1619
DB 2221 CCTTCAAGGGGCTGGGAGAGAGTCAATTTTTTTTGTGAGATCATTTAATTAATG 2280
QY 1620 AATATTTAATTAAGAAATCTAATGAACATTTGAATGTTGCTTAAATGATGATCGG 1679
DB 2281 AATATTTAATTAAGAAATCTAATGAACATTTGAATGTTGCTTAAATGATGATCGG 2340
QY 1680 TTTATGCGAGAGTTTGAAGTTTCTTTTGTGAAAAATTTAGACTTGGGATGACCTTGAG 1739
DB 2341 TTTATGCGAGAGTTTGAAGTTTCTTTTGTGAAAAATTTAGACTTGGGATGACCTTGAG 2400
QY 1740 CAGTAGATATTAACCCCAACAAGCTT 1765
DB 2401 CAGTAGATATTAACCCCAACAAGCTT 2426
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RESULT 2
US-09-068-821-17
Sequence 17, Application US/09068821
Patent No. US2002012969A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method of quantifying tumour
TITLE OF INVENTION: cells in a body fluid and a suitable test kit
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain

```
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PADAT Sequenzmodul Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068.821
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 42 795.5
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 7249-1501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4118 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-068-821-17
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Query Match          50.1%; Score 883.4; DB 10; Length 4118;
Best Local Similarity 97.6%; Pred. No. 1.1e-222;
Matches 950; Conservative 0; Mismatches 16; Indels 7; Gaps 5;

QY 794 GCACGGGCTTGGGAGGCTGGGCGCTGGGAGGGGTGGCCATTCTTCTTAACCTTAA 853
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DB 14 GCGCGGGTGGGAGGCTGGGCGCTGGGAGGGGTGGCCATTCTTCTTAACCTTAA 73
   |||
QY 854 CTGAGAGGGCGTGAAGGCGGCTGCTCCCGCGGGCTGTTTCTCCGCTGACTTT 913
   |||
DB 74 CTGAGAGGGCGCTGAGGCGCGCTGCTTCTCCCGCGGGCTGTTTCTGCTGACTTT 133
   |||
QY 914 CAGCGGGCGGAAAGCCTGCGGCTGCGGCTTCCACCGTTCTATTAAGACAAACAAA 973
   |||
DB 134 CAGCGGGCGGAAAGCCTGCGGCTGCGGCTTCCACCGTTCTATTAAGACAAACAAA 193
   |||
QY 974 ATGTACGCTGTGGCCCGCTTCCCGGGGACCTGCGGGGGTGCCTGCCAGCC 1033
   |||
DB 194 ATGTACGCTGTGGCCCGCTTCCCGGGGACCTGCGGGGGTGCCTGCCAGCC 251
   |||
QY 1034 CCGGAACCCCGCTGAGGCGCGGCTGCGGGGCTTCTCCGGAGGACCTACTGCCA 1093
   |||
DB 252 CCGGAACCCCGCTGGA -GCCGGGGTGGCGCGGGGCTTCTCCGGAGGACCTACTGCCA 310
   |||
QY 1094 CCGGAAGATT -GGCTCTGTGACCGCGGGTCTCTCGGGGGGAGGGGAGGTTGAGGC 1152
   |||
DB 311 CCGGAAGATTGGGCTGTGTGACGGGGGCTCTCGGGGGGAGGGGAGGTTGA -CC 369
   |||
QY 1153 CTTTACGCGCGGAGAGGAGGAGGAGGAGTCCCGCGCGGGCGGCAATTCCTGAGC 1212
   |||
DB 370 GTTTTCAGGCGCGGAGGAGGAGGAGGAGGAGTCCC -GCCCGGGCGCAATTCCTGAGC 427
   |||
QY 1213 TGTGGAGCTGACCGGAGACTGGGCTCAACATGATTCCTTCTCGTTGGTGGGG 1272
   |||
DB 428 TGTGGAGCTGACCGGAGACTGGGCTCAACATGATTCCTTCTCGTTGGTGGGG 487
   |||
QY 1273 GAACGGCGATGCTGCGCATCCGTCAACCCCTCGCGCGGAGTGGGGGCTTGAACCCCA 1332
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DB 488 GAACGGCGATGCTGCGCATCCGTCAACCCCTCGCGCGGAGTGGGGGCTTGAACCCCA 547
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QY 1333 ACCTGACTAGTGGGCGCACTGTGCTGCAAAATTGGGAGAGACGTGAAGGCACTCCAAG 1392
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DB 548 ACCTGACTAGTGGGCGCACTGTGCTGCAAAATTGGGAGAGACGTGAAGGCACTCCAAG 607
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QY 1393 TCGGCCAAATGAAATGGGAGTGAAGCGGGGTTGCCCTGAGCCGTTCCGCTGGGTTCT 1452
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DB 608 TCGGCCAAATGAAATGGGAGTGAAGCGGGGTTGCCCTGAGCCGTTCCGCTGGGTTCT 667
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QY 1453 CCGGCTTCGGCTTTTGTGTCCTTTATGTTGATTAATCAATTAATTCCTGCTGCA 1512
   |||
DB 668 CCGGCTTCGGCTTTTGTGTCCTTTATGTTGATTAATCAATTAATTCCTGCTGCA 727
   |||
QY 1513 GATTTTGTGAGTCTTCTCTCCCAAGGTAGATCTGACACAGTCCCTCAAGGGGT 1572
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DB 728 GATTTTGTGAGTCTTCTCTCCCAAGGTAGATCTGACACAGTCCCTCAAGGGGT 787
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QY 1573 GTGGGAGACAGTCAATTTTGTGAGATCATTTAATTAATTAATTAATTAATTAAG 1632
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DB 788 TGGGAGAACAGTCAATTTTGTGAGATCATTTAATTAATTAATTAATTAATTAAG 847
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QY 1633 AAGATCTAATGAACATTTGGAATTTGTTCTTAATGTCATCGGTTATGCCAGAG 1692
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DB 848 AAGATCTAATGAACATTTGGAATTTGTTCTTAATGTCATCGGTTATGCCAGAG 907
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QY 1693 TTAGAAGTTCTTTTGAATAATTAAGACCTTGGCGATGACCTTAGCGATGATATA 1752
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DB 908 TTAGAAGTTCTTTTGAATAATTAAGACCTTGGCGATGACCTTAGCGATGATATA 967
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QY 1753 CCCCCCAAGCTT 1765
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DB 968 CCCCCCAAGCTT 980
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RESULT 3
US-09-018-125-1
; Sequence 1, Application US/09018125A
; Patent No. US20010007902A1
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Kondo, Seiji
; APPLICANT: Cowell, John K.
; APPLICANT: Li, Guiyang
; APPLICANT: Torrence, Paul F.
; TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
; TITLE OF INVENTION: EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES
; FILE REFERENCE: 8656-022
; CURRENT APPLICATION NUMBER: US/09/018,125A
; CURRENT FILING DATE: 1999-02-03
; EARLIER APPLICATION NUMBER: 60/044,507
; EARLIER FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 962
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-018-125-1
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Query Match          49.9%; Score 881.6; DB 10; Length 962;
Best Local Similarity 73.5%; Pred. No. 1.6e-222;
Matches 711; Conservative 236; Mismatches 14; Indels 7; Gaps 5;

QY 799 GGGTTGCGGAGGCTGGGCTGGGAGGGGCTGGGCAATTTTGTCTAACCTTAAGTGA 858
   |||
DB 1 GGGUUGCGGAGGGUGGCGGCGGAGGGGUGUGGCCAUUUUUUUGUUAACCCUAACUGAG 60
   |||
QY 859 AAGGCGGTAGGCGCGCTGTTTGTCTCCCGCGGCGCTGTTTCTGCTGACTTTGAGG 918
   |||
DB 61 AAGGCGGUAGGCGCGCGUUGUUUGUCUCCCGCGCGUUGUUUUUCUGCGUACUUUCAGCG 120
   |||
QY 919 GGGGGAAGAGCCGCGGCTGCGGCTTCCACGCTTCAATTCATTAAGGCAAAATAATGTC 978
   |||
DB 121 GGGGGAAGAGCCGCGGCTGCGGCGGCGGCGUUCACCGUUUCUUGAGGCAAAATAAUAUUC 180
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QY 979 AGCTGTGCCCCGCTTCCGCGGAGACCTGCGGCGGCTGCGCCACGCCCCGA 1038
 Db 181 AGCTGTGCCCCGCTTCCGCGGAGACCTGCGGCGGCTGCGCCACGCCCCGA 238
 QY 1039 ACCCGCGCTGAGAGCGCGCGCTGCGGCGGCTTCTGCGAGGACCTACTGCGCGG 1098
 Db 239 ACCCGCGCTGAGAGCGCGCGCTGCGGCGGCTTCTGCGAGGACCTACTGCGCGG 297
 QY 1099 AAGAGTT-GGCTGTGAGCGCGGCTGCTGCGGCGGCGGAGGCGAGGCTTCTGCG 1157
 Db 298 AAGAGTGGCGCTGCTGCTGCGGCGGCTGCTGCGGCGGAGGCGAGGCTTCTGCG 356
 QY 1158 AGCGCGAG 1217
 Db 357 AGCGCGAG 414
 QY 1218 GAGCTGACCCAG 1277
 Db 415 GAGCTGACCCAG 474
 QY 1278 CCGATCGTGGCAGTCCGCTGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1337
 Db 475 CCGATCGTGGCAGTCCGCTGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 534
 QY 1338 ACTGACTGGGCGAGTGTGCTGCAAAATTGGCAGAGAGAGAGAGAGAGAGAGAG 1397
 Db 535 ACUGACUGGCGCAGUGUGUGUGCAAAUUGGCGAGAGAGAGAGAGAGAGAGAGAG 594
 QY 1398 CAAATGAATGGGCGAGTGGCGGCGGCTGCGTGGAGAGAGAGAGAGAGAGAGAG 1457
 Db 595 CAAATGAATGGGCGAGTGGCGGCGGCTGCGTGGAGAGAGAGAGAGAGAGAGAG 654
 QY 1458 CTTCGCGCTTTTGTGCTTGTGATGATTAACAATGATGATGATGATGATGAT 1517
 Db 655 CTTCGCGCTTTTGTGCTTGTGATGATTAACAATGATGATGATGATGATGAT 714
 QY 1518 TGTGAGGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1577
 Db 715 TGTGAGGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 774
 QY 1578 AGAAGATGATTTTGTGAGATCATTTATGATTTATGATTTATGATTTATGAT 1637
 Db 775 AGAAGATGATTTTGTGAGATCATTTATGATTTATGATTTATGATTTATGAT 834
 QY 1638 CTAAATGAACATTTGAAATTTGCTTAAATGATGATGATGATGATGATGATG 1697
 Db 835 CTAAATGAACATTTGAAATTTGCTTAAATGATGATGATGATGATGATGATG 894
 QY 1698 AGTTTCTTTTGAATAATTAAGCTTGGCGATGAGCTTGGAGAGAGATTAACCCC 1757
 Db 895 AGTTTCTTTTGAATAATTAAGCTTGGCGATGAGCTTGGAGAGAGATTAACCCC 954
 QY 1758 ACAAGCTT 1765
 Db 955 ACAAGCTT 962

RESULT 4
 US-09-068-821-16
 ; Sequence 16, Application US/09068821
 ; Patent No. us20020012969A1
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Method of quantifying tumour
 ; TITLE OF INVENTION: cells in a body fluid and a suitable test kit
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & Mcclain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PADAT sequenzmodul Version 1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/068.821
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: DE 195 42 795.5
 FILING DATE: 16-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619)238-0999
 TELEFAX: (619)238-0062
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 962 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 US-09-068-821-16

Query Match 49.9%; Score 881.6; DB 10; Length 962;
 Best Local Similarity 97.8%; Pred. No. 1.6e-222;
 Matches 947; Conservative 0; Mismatches 14; Indels 7; Gaps 5;

QY 799 GGGTGGCGGAGGCGGCTTGGGAGAGGCGGCTGATTTTGTCTAACCCTAAGTAG 858
 Db 1 GGGTGGCGGAGGCGGCTTGGGAGAGGCGGCTGATTTTGTCTAACCCTAAGTAG 60
 QY 859 AAGGCGGTAGGCGGCGGCTTGGGAGAGGCGGCTGATTTTGTCTAACCCTAAGTAG 918
 Db 61 AAGGCGGTAGGCGGCGGCTTGGGAGAGGCGGCTGATTTTGTCTAACCCTAAGTAG 120
 QY 919 GGGGAGAAAGCGTGGCGCTGCGGCTTCCACCGCTTCTAGAGCAAAAGAAATGTC 978
 Db 121 GGGGAGAAAGCGTGGCGCTGCGGCTTCCACCGCTTCTAGAGCAAAAGAAATGTC 180
 QY 979 AGCTGCTGGCGGCTTGGCGGCTTCCGCGGAGCTGCGGCGGCTGCGGCGGCGG 1038
 Db 181 AGCTGCTGGCGGCTTGGCGGCTTCCGCGGAGCTGCGGCGGCTGCGGCGGCGG 238
 QY 1039 ACCCGCGCTGAGAGCGCGGCTGCGGCGGCTTCTCCGAGAGAGAGAGAGAGAGAG 1098
 Db 239 ACCCGCGCTGAGAGCGCGGCTGCGGCGGCTTCTCCGAGAGAGAGAGAGAGAGAG 297
 QY 1099 AAGAGTT-GGCTGTGAGCGCGGCTGCTGCGGCGGCGGAGGCGAGGCTTCTGCG 1157
 Db 298 AAGAGTGGCGCTGCTGCTGCGGCGGCTGCTGCGGCGGAGGCGAGGCTTCTGCG 356
 QY 1158 AGCGCGAG 1217
 Db 357 AGCGCGAG 414
 QY 1218 GAGCTGACCCAG 1277
 Db 415 GAGCTGACCCAG 474
 QY 1278 CCGATCGTGGCAGTCCGCTGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1337
 Db 475 CCGATCGTGGCAGTCCGCTGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 534
 QY 1338 ACTGACTGGGCGAGTGTGCTGCAAAATTGGCAGAGAGAGAGAGAGAGAGAGAGAG 1397
 Db 535 ACTGACTGGGCGAGTGTGCTGCAAAATTGGCAGAGAGAGAGAGAGAGAGAGAGAG 594
 QY 1398 CAAATGAATGGGCGAGTGGCGGCGGCTGCGTGGAGAGAGAGAGAGAGAGAGAG 1457

Db 595 CAAATGATGCGAGTACCGCGGGTTCCTGAGCCGTTCCCTGCGGTTCTCCCGT 654
QY 1458 CTTCCGCTTTTGTGCTTTTATGTTGATTACAACTTATGTTCTGCTGAGATT 1517
Db 655 CTTCCGCTTTTGTGCTTTTATGTTGATTACAACTTATGTTCTGCTGAGATT 714
QY 1518 TGTGAGGTTTGTGCTTTTCCCAAGTAGATCTGACACAGTCCCTCAACGGGGTGGG 1577
Db 715 TGTGAGGTTTGTGCTTTTCCCAAGTAGATCTGACACAGTCCCTCAACGGGGTGGG 774
QY 1578 AGAAGCTATTTTGTGAGATCATTTAACTTTAATGATTTAATGAGAAT 1637
Db 775 AGAAGCTATTTTGTGAGATCATTTAACTTTAATGATTTAATGAGAAT 834
QY 1638 CTAATGACATTTGAAATGTCTCTTAAATGATCATGTTTATGCGAGGTTAGA 1697
Db 835 CTAATGACATTTGAAATGTCTCTTAAATGATCATGTTTATGCGAGGTTAGA 894
QY 1698 AGTTCTTTTGTGAAATATGACCTTGGGATGACCTTGGAGAGTATTAACCCC 1757
Db 895 AGTTCTTTTGTGAAATATGACCTTGGGATGACCTTGGAGAGTATTAACCCC 954
QY 1758 ACAAGCTT 1765
Db 955 ACAAGCTT 962

RESULT 5
US-09-068-821-20
Sequence 20, Application US/09068821
Patent No. US20020012969A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method of quantifying tumour
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McElain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PADAT Sequenzmodul Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,821
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 42 795.5
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 7249-1501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0062
TELEFAX: (619)238-0062
INFORMATION FOR SEQ. ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic RNA
US-09-068-821-20

Query Match 47.7%; Score 841.6; DB 10; Length 975;
Best local Similarity 71.3%; Pred. No. 5.3e-212;
Matches 690; Conservative 232; Mismatches 39; Indels 7; Gaps 5;

QY 794 GCACCGGTTGCGAGAGGTGGCCCTGGAGAGGGGNGGCCATTTTGTGCTAACCCCTAA 853
Db 14 GCGCGGGGUGCGGAGAGGUGGCGCUGGAGAGGGUGGCGCAUUDUUUGCUAAACCUAA 73
QY 854 CTGAGAGGGCGTAGGCGCCGCTTGTGCTCCCGCGCGCTGTGTTTCTGCGTGAATT 913
Db 74 CUGAGAGGGCGUAGGCGCGCGCUUUGUCUCCCGCGCGCUUUUUUUUCUGGUGACUU 133
QY 914 CAGCGGGCGGAAAAACCTCGGCTGCCCGCTTCCACCCTTCACTTCTAGACAAACAAA 973
Db 134 CAGCGGGCGGAAAAACCTCGGCGCGCGCUUUCACCGGUCUUAUUGAGCAAAACAAA 193
QY 974 ATGACAGCTGCTGGCCGCTTGTGCTGCGGGGACCTGCGGGGGGCGCTGCCCGACC 1033
Db 194 AUGGACAGCTGCGCGCGCTTGTGCTGCGGGGACCTGCGGGGGGCGCTGCCCGACC 251
QY 1034 CCGGAACCCCGCTGAGAGCGCGGCTGCGCGCGCGCGCTTCCGAGAGCACTACTGCCA 1093
Db 252 CCGGAACCCCGCTGAGAGCGCGGCTGCGCGCGCGCGCTTCCGAGAGCACTACTGCCA 310
QY 1094 CCGGGAAGATT-GGCTCTGTCAAGCGCGGCTCTCTGCGGGCGAGGGCGAGTTCAAGC 1152
Db 311 CCGGGAAGAGUUGGGGCUUCUACAGCCGCGGUCUCUGGGGGGAGGGCGAGGUCA-CC 369
QY 1153 CTTTCAGGGCGCGAG 1212
Db 370 GUUDCAAGCGCGAG 427
QY 1213 TGTGAGAGCTGACCCAG 1272
Db 428 UUGGAGAGGAG 487
QY 1273 GAAAGCGATGTCGAGATCCGTCACCCCTGCGCGCGAGAGAGAGAGAGAGAGAG 1332
Db 488 GAAAGCGAG 547
QY 1333 ACCTGACAGTGGGCGAG 1392
Db 548 ACCUGAG 607
QY 1393 TCGGCGCAATGAG 1452
Db 608 GCGGAG 667
QY 1453 CCGGCTTCCGCTTTTGTGCTTTTATGTTGATTTACACTTATGTTCTGCTGCA 1512
Db 668 CCGGCTTCCGCTTTTGTGCTTTTATGTTGATTTACACTTATGTTCTGCTGCA 727
QY 1513 GATTTGTTAGGTTTGTGCTTTTCCCAAGTAGATCTGACACAGTCCCTCAACGGGGT 1572
Db 728 GAUUDUUUGGUGUUGGUGUUGGUGUUGGUGUUGGUGUUGGUGUUGGUGUUGGUGU 787
QY 1573 GTGGAG 1632
Db 788 UGGGAG 847
QY 1633 AAGATCTAATGAACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1692
Db 848 AAGATCTAATGAACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 907
QY 1693 TTAGAGATTTCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1752
Db 908 UUGAG 967
QY 1753 CCGGCAACA 1760
Db 968 CCGGCAACA 975

RESULT 6
US-09-068-821-18
Sequence 18, Application US/09068821


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QY 1034 CCGGAACCCCGCTGAGAGCCGCGCTGCGCCGGGCTTCTCGAGAGCACTACTGCA 1093
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Db 252 CCGGAACCCCGCTGAGAGCCGCGCTGCGCCGGGCTTCTCGAGAGCACTACTGCA 310
QY 1094 CCGCGAAGATT-GGCTCTGACAGCCGCGGCTCTCTGGGGGAGGCGAGTTGAGGC 1152
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 311 CCGCGAAGATTGGGCTCTCTGAGAGCCGCGGCTTCTCTGGGGGAGGCGAGTTGAGGC 369
QY 1153 CTTTCAAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1212
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Db 370 GUUUCAGAGCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
QY 1213 TGTGGAGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1272
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Db 428 UGUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
QY 1273 GAACGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1332
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Db 488 GAACGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
QY 1333 ACCTGAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1392
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Db 548 ACCTGAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
QY 1393 TCGGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1452
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Db 608 CUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
QY 1453 CCGGCTGCGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1512
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Db 668 CCGGCTGCGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1572
QY 1513 GATTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1572
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Db 728 GAUUGUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
QY 1573 GTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1632
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Db 788 UGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
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Db 848 AGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
QY 1693 TTAGAAGTTCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1752
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Db 908 UAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
QY 1753 CCGGCGACA 1760
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Db 968 CCGGCGACA 975

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-09-057-351-1

Query Match      31.0%; Score 546.4; DB 10; Length 560;
Best Local Similarity 80.7%; Pred. No. 2,1e-134;
Matches 452; Conservative 106; Mismatches 1; Indels 1; Gaps 1;

QY 799 GGGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858
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Db 1 GGGUUGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 859 AAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
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Db 61 AAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 919 GGGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978
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Db 121 GGGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 979 AGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
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Db 181 AGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 1039 ACCCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
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Db 241 ACCCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 1099 AAGAGTT-GGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1157
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Db 301 AAGAGTTGGGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 1158 AGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1217
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Db 361 AGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 1218 GACGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1277
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Db 421 GACGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 1278 CCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1337
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 CCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 1338 ACTGACTGGGCGACAGTGTGCT 1357

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RESULT 9
US-09-057-351-1
Sequence 1, Application US/09057351
Patent No. US2001003439A1
GENERAL INFORMATION:
APPLICANT: Villaponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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Db 541 ACUGACUGGCGCAGUGUCU 560

RESULT 10

US-09-835-232-6/c
; Sequence 6, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Phillip
; APPLICANT: Leder, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; PRIORITY FILING DATE: 2001-04-12
; PRIORITY FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-09-835-232-6

Query Match 5.8%; Score 101.8; DB 10; Length 180216;

Best Local Similarity 88.5%; Pred. No. 4,4e-16; Indels 4; Gaps 1;

Matches 123; Conservative 0; Mismatches 12; Indels 4; Gaps 1;

Db 64485 AGCTACTCAGAGAGCTGAGACAGAGATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60

1 AGCTACTCAGAGAGCTGAGACAGAGATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60

64425 AGCGGAGATCGCGCCACTACAC---TCCAGCTGGGCAACAGACGAGCTCCGTCTCA 64370

121 AAAAAAAAAAATCGTTACAA 139

64369 AAAAAAAAAAATGTATA 64351

RESULT 11

US-09-764-877-2623/c
; Sequence 2623, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; PRIORITY FILING DATE: 2001-01-17
; PRIORITY FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2623
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2623

Query Match 5.7%; Score 101.2; DB 10; Length 32193;

Best Local Similarity 86.2%; Pred. No. 2,7e-16; Indels 0; Gaps 0;

Matches 112; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 31984 ACCTACTCAGAGAGCTGAGACAGAGATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60

1 AGCTACTCAGAGAGCTGAGACAGAGATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60

31984 ACCTACTCAGAGAGCTGAGACAGAGATCGTTGAACCCGGAGGAGGAGTTGCAGTG 31925

QY 61 AGCGAGATCAGCGCCACTAGATCCATCCAGCCTGGGCGAAGAGCAAGACTCCGTCTCA 120

31924 AGCTGAGATCGTGCCTGACCTGACCTGAGCCTGGGCAACAGATAGACTTATCTCA 31865

121 AAAAAAAAAA 130

31864 AAAAAAAAAA 31855

RESULT 12

US-09-263-959-1/c
; Sequence 1, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-MAR-1999
; APPLICATION NUMBER: US/09/263,959
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
US-09-263-959-1

Query Match 5.7%; Score 101.2; DB 10; Length 684973;

Best Local Similarity 86.2%; Pred. No. 1,2e-15; Indels 0; Gaps 0;

Matches 112; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCTACTCAGAGAGCTGAGACAGAGATCGTTGAACCCGGAGGAGGAGTTGCAGTG 60

442801 AGCTACTCAGAGAGCTGAGACAGAGATCGTTGAACCCGGAGGAGGAGTTGCAGTG 442742

61 AGCGAGATCAGCGCCACTAGATCCATCCAGCCTGGGCGAAGAGCAAGACTCCGTCTCA 120

442741 AGCGAGATCGTGCCTGACCTGACCTGAGCCTGGGCAACAGATAGACTTATCTCA 442682

121 AAAAAAAAAA 130

442681 AAAAAAAAAA 442672

RESULT 13

US-09-962-832-154/c
; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:

RESULT 15
US-09-764-904-71/c

Search completed: December 19, 2002, 15:13:48
Job time : 1612 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 2130 Seconds

(without alignments)
13420.204 Million cell updates/sec

Title: US-09-601-267-1

Perfect score: 1765
Sequence: 1 agcactcagagagcgtcaga.....gataataccccacacagctt 1765

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estcda:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
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14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
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19: em_gss_hum:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rpod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	424.2	24.0	443 9	AI825849 tdl9d01.x
2	390.8	22.1	421 10	AM293800 UT-H-B12-
3	371.4	21.0	412 10	AM136367 UT-H-B11-
4	355.4	20.1	376 9	AI180754 tlf97g05.x
5	355.2	20.1	388 10	AM207347 UI-H-B11-
6	351.4	19.9	353 14	BM695101 UI-E-CL1-BM695101

Result No.	Score	Query Match Length	DB ID	Description
7	110.8	6.3	466 17	AQ229478 HS-2021-A
8	109.2	6.2	680 17	AG186502 Pan tTrog1
9	107.6	6.1	418 17	AQ390169 CITR1-E1-
10	107.2	6.1	469 13	BM509394 h117f10.Y
11	107.2	6.1	516 13	B1468297 1487b01.Y
12	107.2	6.1	529 14	BQ270800 1K05b06.Y
13	107.2	6.1	556 14	BQ267333 1K02c03.Y
14	107.2	6.1	589 14	BQ270346 1K09g10.Y
15	106.4	6.0	635 17	AQ428429 CITR1-E1-
16	106	6.0	774 17	AQ751486 HS-357-B
17	104.8	5.9	671 17	AQ418931 RPCI-11-1
18	104.6	5.9	465 17	AQ527107 CITR1-E1-
19	104.6	5.9	815 14	BQ429052 AGENCOURT
20	104.4	5.9	303 14	BM672404 UI-E-CQ0-
21	104.4	5.9	712 17	AG139751 Pan tTrog1
22	103.8	5.9	451 14	N66929 za47h09.s1
23	103	5.8	837 13	B1820230 603037070
24	103	5.8	1074 14	BQ429712 AGENCOURT
25	102.8	5.8	318 13	B1492686 dE27908.w
26	102.8	5.8	340 10	AM021747 dE27908.Y
27	102.8	5.8	684 17	AG109444 Pan tTrog1
28	102	5.8	364 17	AQ333390 HS-5010-A
29	101.6	5.8	256 9	AA084337 zn04b05.s
30	101.2	5.7	382 10	AV764523 AV764523
31	101.2	5.7	474 9	A1866580 tE51c10.x
32	101.2	5.7	514 17	B37536 HS-1044-A1-
33	101.2	5.7	735 9	AU120382 AU120382
34	101.2	5.7	773 12	BG221771 RST41586
35	101.2	5.7	815 12	BF382750 601816513
36	101.2	5.7	859 17	AQ750588 HS-5573-B
37	101.2	5.7	925 12	BG249993 602362061
38	101	5.7	445 17	AQ198078 RPCI11-46
39	100.4	5.7	504 9	AI138096 DKFZPS47B
40	100.2	5.7	335 9	AA492202 ng78e08.s
41	100	5.7	459 17	AQ483064 RPCI-11-2
42	99.8	5.7	460 14	W07861 zB04q03.r1
43	99.8	5.7	404 9	A1597733 tU91a08.x
44	99.8	5.7	464 10	AW150226 xg49d01.x
45	99.8	5.7	662 17	AQ262070 CITR1-E1-

ALIGNMENTS

RESULT 1
AI825849/c 443 bp mRNA linear EST 24-AUG-1999
LOCUS tdl9d01.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2076097 3',
DEFINITION mRNA sequence.
ACCESSION AI825849
VERSION AI825849.1 GI:5446520
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 443)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strassberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers

FEATURES

	source	1. 443	/organism="Homo sapiens"	
			/db_xref="taxon:9606"	
			/clone="IMAGE:2076097"	
			/clone_lib="NCI_CGAP_Col6"	
			/tissue_type="colon tumor, RER+"	
			/lab_host="DH10B"	
			/note="Organ: colon; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not T; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP-Col6 was prepared, and ss circles were made in vitro. Following HATP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1057416-106125, and 1144584-114531)."	
			Subtraction by Bento Soares and M. Fatima Bonafide.	
BASE COUNT	78 a	144 c	151 g	68 t 2 others
ORIGIN				
Query Match		24.0%	Score 424.2;	DB 9; Length 443;
Best Local Similarity		98.6%	Pred. No. 1.7e-94;	
Matches 437:	Conservative	0;	Mismatches 5;	Indels 1; Gaps 1;
OY	895	TCTTTTTCCTGCCTGACTTTCACGGGGCGAAAAAGCCTCGCCCTCCCTCACCGTTTC	954	
Db	443	TTTTTTTTCCTGGTGACTTTCACGGGGCGAAAAAGCCTCGCCCTCCCTCACCGTTTC	384	
OY	955	ATTCTAGACAACAATAAATGTCAAGCTGTGSCCGTTCCGCCCTCCCGGGGACCCTGGC	1014	
Db	383	ATTCTAGACAACAATAAATGTCAAGCTGTGSCCGTTCCGCCCTCCCGGGGACCCTGGC	324	
OY	1015	GCGGGTCGCGTCCGCCAGCCCCGAACCCCGCCTGAGAGCCGCGGTGCGCCCGGGGCTTCT	1074	
Db	323	GCGGGTCGCGTCCGCCAGCCNCCGAAACNCCGCTCGGAGGCGCGGTGCGCCCGGGGCTTCT	264	
OY	1075	CGGAGGGACCTACTGACCGAACCGCGGAAGAATT-GGCTGTGTACAGCCGGGGGTCTTCGGGG	1133	
Db	263	CGGAGGGACCTACTGACCGAACCGCGGAAGAATTGGCTGTGTACAGCCGGGGGTCTTCGGGG	204	
OY	1134	GCGAGGGGAGGTTTCAGGCTTTCAGGGCGCAGAAAGAGAGAGAGAGAGAGTCCCGCGGC	1193	
Db	203	GCGAGGGGAGGTTTCAGGCTTTCAGGGCGCAGAAAGAGAGAGAGAGAGTCCCGCGGC	144	
OY	1194	GCGGGGCAATTCCTCGAGCTGTGGGACGTGGACCCAGAACTGGCTCACACATGCAATTC	1253	
Db	143	GCGGGGCAATTCCTCGAGCTGTGGGACGTGGACCCAGAACTGGCTCACACATGCAATTC	84	
OY	1254	GCTTTCCTGTGGTGGGGGGAACGCGCATTCGCGCATTCGACCCCTCGCGGGCAGTG	1313	
Db	83	GCTTTCCTGTGGTGGGGGGAACGCGCATTCGCGCATTCGACCCCTCGCGGGCAGTG	24	
OY	1314	GGGGCTTGTGAACCCCAAACT 1336		
Db	23	GGGGCTTGTGAACCCCAAACT 1		
RESULT 2				
LOCUS	AM293800/c			
DEFINITION	UI-H-B12-shp-f-04-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens CDNA clone	421 bp	mRNA	linear EST 16-JAN-2000
ACCESSION	AM293800			
VERSION	AM293800.1	GI:6700436		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
	Unpublished (1997)			

[illegible]

|||||
 Db 301 AACAAAAATGTCAGCTGCGCCGCTTCCGCGGAGCAGTCGGCGGCT 242
 1026 GCCCAGCCCCGAAACCCCGCTGAGAGCCGCGGCTCGGCCGCTTCTCCGAGGCACC 1085
 Db 241 GCGCCACCCCGGAAACCCCGCTGAGAGCCGCGGCTCGGCCGCTTCTCCGAGGCACC 182
 1086 TACTGCACCGCAGAGATT-GGCTCTGTTCAGCGCGGCTCTCTCGGGGCGAGGGCGAG 1144
 Db 181 CACTGCCACCGCAGAGATTGGGCTCTGTTCAGCGCGGCTCTCTCGGGGCGAGGGCGAG 122
 1145 GTTTCAGCGCTTTCAGCGCGCAGAGAGAAAGAGAGAGTCCCGCGCGCGCGATT 1204
 Db 121 GTTCAGGCGCTTTCAGCGCGCAGAGAGAGAGAGAGAGTCCCGCGCGCGCGATT 62
 1205 CCTGAGCTGTGGAGCTGACCCAGAGCTCGGCTCACACATGCAG 1250
 Db 61 CCTGAGCTGTGGAGCTGACCCAGAGAGTCTGCTCACATGCAG 16

RESULT 3
 AM136367/c 412 bp mRNA linear EST 29-OCT-1999
 LOCUS UI-H-B11-acn-h-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
 DEFINITION IMAGE:2715099 3', mRNA sequence.
 ACCESSION AM136367
 VERSION AM136367.1 GI:6140500
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 412)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgarbs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first A
 tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
 NCI_CGAP clone distribution information can be found through the
 I.M.A.G.E. Consortium/ILNL at:
 www.bio.livl.gov/birp/image.html The following repetitive
 elements were found in this cDNA sequence: 200-276,
 >GC_rich#low-complexity
 Seq primer: M13 Forward
 POLYA=yes.

FEATURES
 source Location/Qualifiers

1..412
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2715099"
 /lab_host="NCI_CGAP_Sub3"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NCI_CGAP_Sub3 library is a subtracted library derived from
 the NCI_CGAP_Sub1 library, which is a subtracted library
 derived from B1. B1 constitutes a mixture of 21
 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4
 , NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
 NCI_CGAP_Co16, NCI_CGAP_Kid3, NCI_CGAP_Kid12,
 NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
 NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CUL1, NCI_CGAP_Le12,
 NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
 NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
 NCI_CGAP_Brn25. These 21 libraries were pooled and a
 single-stranded DNA preparation of the resulting mixture
 was used as a tracer in a subtractive hybridization with
 a driver whose composition is detailed below:

NCI_CGAP_Kid3 pool 1 LLM 3334-3337, 3682-3683,
 3798-3803 (IMAGE Clones 1322376-1323911, 1456008-1456775
 , 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLM 3338-3342
 , 3722-3725, 3776-3778 (IMAGE Clones 1333912-1325831,
 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
 LLM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991,
 1520904-1522439); NCI_CGAP_GC4 pool 1 LLM 3164-3167,
 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631,
 1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
 LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones
 985608-986759, 1101192-1101959, 1217928-1220615);
 NCI_CGAP_Co10 pool 1 LLM 2644-2653, 2871-2872 (IMAGE
 Clones 1057416-1061255, 114584-114531). Subtraction
 was performed as previously described [Bonaldi, Lennon &
 Soares (1996): Normalization and Subtraction. Two
 Approaches to Facilitate Gene Discovery. Genome Research
 6, 791-806.
 TAG_Lib=NCI_CGAP_Co10
 TAG_Tissue=colon
 TAG_SEQ=NAACG"

BASE COUNT 66 a 132 c 140 g 74 t
 ORIGIN
 Query Match 21.0%; Score 371.4; DB 10; Length 412;
 Best Local Similarity 99.5%; Pred. No. 2, 1e-81;
 Matches 383; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 868 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 927
 Db 402 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 343
 QY 928 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 987
 Db 342 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 283
 QY 988 CCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 1047
 Db 282 CCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 223
 QY 1048 GAGAGCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 1106
 Db 222 GAGAGCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 163
 QY 1107 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 1166
 Db 162 GCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 103
 QY 1167 GAGAGCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 1226
 Db 102 GAGAGCGCGCGCTGTTTGTCTCCCGCGCGCTGTTTCTGCTGACTTTCAGCGCGGAGAAA 43
 QY 1227 CCGAGCTCGGCTCACATGCAGT 1251
 Db 42 CCGAGCTCGGCTCACATGCAGT 18

RESULT 4
 A1380754/c 376 bp mRNA linear EST 30-MAR-1999
 LOCUS Lf97905.x1 NCI_CGAP_CUL1 Homo sapiens cDNA clone IMAGE:2107256 3',
 DEFINITION mRNA sequence.
 ACCESSION A1380754
 VERSION A1380754.1 GI:4190607
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 376)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 479 Std Error: 0.00
Seq primer: -400P from Glibco.

FEATURES

source

Location/Qualifiers
1. 376
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2107256"
/clone_id="NCI-CGAP-CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand CDNA
was primed with a Not I oligo(dT) primer [5'
TCTTACCAATCTGAGAGGGAGCGCCGCGATTCTTTTCTTTTCTTTT
T 3'] double-stranded CDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT
ORIGIN

60 a 122 c 133 g 61 t

Query Match

Best Local Similarity 99.5%; Pred. No. 2e-77; Length 376;
Matches 367; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 883 CTCGCCGCGCGCTTTTTCCTGCTTCAAGCGGCGAAAGCCTGGCCTGCCGC 942
DB 376 CTCGCCGCGCGCTTTTTCCTGCTTCAAGCGGCGAAAGCCTGGCCTGCCGC 317
OY 943 CTTCACACGCTTCTAGAGCAAAATAATGTAGCTGCTGCGCCGCTTCCCTCC 1002
DB 316 CTTCACACGCTTCTAGAGCAAAATAATGTAGCTGCTGCGCCGCTTCCCTCC 257
OY 1003 CGGGGACCTGCGGCGCTGCTGCCAGCCCGGAACCCGCTGGAGCCCGGTCG 1062
DB 256 CGGGGACCTGCGGCGCTGCTGCCAGCCCGGAACCCGCTGGAGCCCGGTCG 197
OY 1063 CGGGGCGCTTCTCGAGAGCACTACTGCGACCGCGAAGATT-GGCTCTGTACCGCG 1121
DB 196 CGGGGCGCTTCTCGAGAGCACTACTGCGACCGCGAAGATTGGCTCTGTACCGCG 137
OY 1122 GGTCTCTCGGGGCGAGAGGCGAGTTCAGCCCTTTCAGGCGCGAGAGAGAGGAG 1181
DB 136 GGTCTCTCGGGGCGAGAGGCGAGTTCAGCCCTTTCAGGCGCGAGAGAGAGGAG 77
OY 1182 GATGTCCTGCGCGCGCGCGCGATTCCTGTGAGCTGTGGAGCTGACCCAGACTCGCTCA 1241
DB 76 GATGTCCTGCGCGCGCGCGCGATTCCTGTGAGCTGTGGAGCTGACCCAGACTCGCTCA 17
OY 1242 CACATGCAG 1250
DB 16 CACATGCAG 8

RESULT 5

AN207347/c

LOCUS

DEFINITION AM207347 388 bp mRNA linear EST 02-DEC-1999

IMAGE:2723056-3', mRNA sequence.

ACCESSION AM207347

VERSION AM207347.1 GI:6506843

KEYWORDS EST.

SOURCE

ORGANISM

human.

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 388)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand CDNA and therefore this may represent a bonafide poly A
tail. CDNA Library Preparation: M.B. Soares lab clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this CDNA sequence: 286-362,
>GC-rich#Low-complexity
Seq primer: M13 forward
POLYA=Yes.

FEATURES

source

Location/Qualifiers
1. 388
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2723056"
/clone_id="NCI-CGAP-Sub3"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site.1: Not I; Site.2: Eco RI; The
NCI-CGAP-Sub3 library is a subtracted library derived from
the NCI-CGAP-Sub1 library, which is a subtracted library
derived from B1. B1 constitutes a mixture of 21
normalized or subtracted NCI-CGAP libraries: NCI-CGAP-Co4
, NCI-CGAP-Pr22, NCI-CGAP-Pr28, NCI-CGAP-Co10,
, NCI-CGAP-Co16, NCI-CGAP-Kid5, NCI-CGAP-Kid12,
NCI-CGAP-Kid3, NCI-CGAP-Kid11, NCI-CGAP-Lym2,
NCI-CGAP-Bf2, NCI-CGAP-Co8, NCI-CGAP-CLL1, NCI-CGAP-Le12,
NCI-CGAP-Bf23, NCI-CGAP-Lu5, NCI-CGAP-Lu24,
NCI-CGAP-Lu19, NCI-CGAP-GC4, NCI-CGAP-GC6,
NCI-CGAP-Bf25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI-CGAP-Kid3 pool 1 LLM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonoids 132376-132391, 145608-1456775
, 1500552-1502855); NCI-CGAP-Kid5 pool 1 LLM 3338-3342
, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831,
1471368-1472903, 1492104-1493255); NCI-CGAP-Lu5 pool 1
LLM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991,
1520904-1522439); NCI-CGAP-GC4 pool 1 LLM 3164-3167,
3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631,
1469064-1470983, 1475592-1476743); NCI-CGAP-Pr22 pool 1
LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids
985608-986759, 1101192-1101959, 1217928-1220615);
NCI-CGAP-Co10 pool 1 LLM 2644-2653, 2871-2872 (IMAGE
Clonoids 1057416-1061255, 1145584-1145351). Subtraction
was performed as previously described [Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG-LIB=NCI-CGAP-Co10
TAG-TISSUE=colon
TAG-SEQ=AAACG-

BASE COUNT
ORIGIN

58 a 127 c 132 g 71 t

Query Match

Best Local Similarity 98.9%; Pred. No. 2.2e-77;
Matches 368; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 968 CAAAATAATGTCAGCTGCTGCGCCGCTCCCGGAGACCTGCGGCGGCTGCCCTGC 1027

```
|||||
Db 388 CAAAATATCTACACTGTGGCCGCTTGCCTCCGCGGAGACCTGCGGCGGGTGCCTGC 329
1028 CAGACCCCGGACCCCGCTTGGAGCGCGGCTGCGCCCGGGGCTTCTCCGAGGACCTA 1087
328 CAGACCCCGGACCCCGCTTGGAGCGCGGCTGCGCCCGGGGCTTCTCCGAGGACCTA 269
1088 CTCACACCGGAGAGATT-GGCTCTGTACACCGCGGGTCTCTCGGGGGCGAGGGAGGT 1146
268 CTCACACCGGAGAGATTGGGCTCTGTGTACACCGCGGGTCTCTCGGGGGCGAGGGAGGT 209
1147 TCAGGCTTTTCAGCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
208 TCAGGCTTTTCAGCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 149
1207 CTGAGCTTGGGAGCTGACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1266
148 CTGAGCTTGGGAGCTGACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 89
1267 TGGGGGGAACCGGATCGTCCGATCCGTCACCCCTGCGCGGAGAGTGGGGCTTGTGAAC 1326
88 TGGGGGGAACCGGATCGTCCGATCCGTCACCCCTGCGCGGAGAGTGGGGCTTGTGAAC 29
QY 1327 CCCCCAACCTGA 1338
Db 28 CCCCCAACCTGA 17

RESULT 6
BM695101/c 353 bp mRNA linear EST 28-FEB-2002
LOCUS UI-E-CL1-aez-h-03-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone
DEFINITION UI-E-CL1-aez-h-03-0-UI 5', mRNA sequence.
ACCESSION BM695101
VERSION BM695101.1 GI:19008359
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 353)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
COMMENT 97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1. 353
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UI-E-CL1-aez-h-03-0-UI"
/clone_id="UI-E-CL1"
/tissue_type="human retina"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CL1 is a normalized cDNA library containing the
following tissue(s): retina. The library was constructed
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|||||
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CCGCG. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
BASE COUNT 111 a 88 c 74 g 80 t
ORIGIN
Query Match 19.9%; Score 351.4; DB 14; Length 353;
Best Local Similarity 99.7%; Pred. No. 1,9e-76;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1323 GAACCCCGGACCGTGAAGTGGGCGGAGTGTGTCGCAAAATTGGCAGAGACGGAAGGC 1382
11 |||||
Db 353 GAGCCCGCAACCTGACTGACTGGCCAGTGTGTGCAAAATTGGCAGAGACGGAAGGC 294
1383 ACCTCCAAAGTCGGCCAAATGAATGAATGGGAGAGCCGGGTTGCTGTGAGCCGTTCTG 1442
293 ACCTCCAAAGTCGGCCAAATGAATGAATGGGAGAGCCGGGTTGCTGTGAGCCGTTCTG 234
QY 1443 CGTGGCTTCCCGCTCTCCGCTTTTGTGCTTTATGTTATGATTAACCTACTTC 1502
233 CGTGGCTTCCCGCTCTCCGCTTTTGTGCTTTATGTTATGATTAACCTACTTC 174
QY 1503 CTCCTCTGCAAGATTTTGTAGGTTTTCCTCCCAAGTATGATTCAGCAGTCCCG 1562
11 |||||
Db 173 CTGCTCTGCAAGATTTTGTAGGTTTTCCTCCCAAGTATGATTCAGCAGTCCCG 114
QY 1563 TCAACGGGGTGTGGAGACATCATTTTGTGAGAGATCATTTAACAATTGAAT 1622
113 TCAACGGGGTGTGGAGACATCATTTTGTGAGAGATCATTTAACAATTGAAT 54
QY 1623 ATTTAATTGAAGATCTTAATGAACATTTGATTTGTTTATGATTCGA 1675
53 ATTTAATTGAAGATCTTAATGAACATTTGATTTGTTTATGATTCGA 1
Db 53 ATTTAATTGAAGATCTTAATGAACATTTGATTTGTTTATGATTCGA 1

RESULT 7
AO229478/c 466 bp DNA linear GSS 26-SEP-1998
LOCUS HS_2021_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=2021 COL=16 Row=A, DNA sequence.
ACCESSION AO229478
VERSION AO229478.1 GI:3654707
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,D., Young,D., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT 99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2021 row: A column: 16
Class: BAC ends
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High quality sequence stop: 466.

FEATURES
Location/Qualifiers
source 1..466
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="2021 Col=16 Row=A"
/clone_lib="CIR Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones In E-Coli DH10B"

BASE COUNT 113 a 94 c 111 g 147 t 1 others

ORIGIN

Query Match
Best Local Similarity 90.8%; Score 110.8; DB 17; Length 466;
Matches 118; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 AGCTACTCAGGAGGCTGACACGAGAAATCGCTTGAAACCGGAGGAGGAGGTTGCAGTG 60
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Db 399 AGCTACTCAGGAGGCTGAGGAGGAATCACTTGAAACCGGAGGAGGTTGCAGTG 340
|||||

OY 61 AGCCGAGATCAGCGGCTAGACTCCATCCAGCTGGGCGAAGAGCAAGACTCCGCTCA 120
|||||
Db 339 AGCCGAGATCAGCGGCTAGACTCCATCCAGCTGGGCGAAGAGCAAGACTCCGCTCA 280
|||||

OY 121 AAAAAAAAAA 130
|||||
Db 279 AAAAAAAAAA 270
|||||

RESULT 8
AC186502 680 bp DNA linear GSS 09-JAN-2002
DEFINITION Pan troglodytes DNA, clone: RP43-060015.T7, genomic survey
sequence.
AC186502
VERSION AG186502.1 GI:16716182
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-060015.T7.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE BAC end sequences of Library RPCI-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 680)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
(E-mail:chimpesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..680
/organism="Pan troglodytes"
/db_xref="taxon:9606"
/clone="RP43-060015.T7"
/sex="male"
/cell_type="lymphocytes"

/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

BASE COUNT 194 a 156 c 163 g 121 t 46 others

ORIGIN

Query Match
Best Local Similarity 87.0%; Score 109.2; DB 17; Length 680;
Matches 120; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 1 AGTACTCAGGAGGCTGAGACAGAAATCGCTTGAAACCGGAGGAGGAGGTTGCAGTG 60
|||||
Db 239 AGTACTCAGGAGGCTGAGACAGAAATCGCTTGAAACCGGAGGAGGTTGCAGTG 298
|||||

OY 61 AGCCGAGATCAGCGGCTAGACTCCATCCAGCTGGGCGAAGAGCAAGACTCCGCTCA 120
|||||
Db 299 AGCCGAGATCAGCGGCTAGACTCCATCCAGCTGGGCGAAGAGCAAGACTCCGCTCA 358
|||||

OY 121 AAAAAAAAAATCGTTACA 138
|||||
Db 359 AAAAAAAAAAAGAAAAA 376
|||||

RESULT 9
AO390169 418 bp DNA linear GSS 06-MAR-1999
LOCUS AO390169
DEFINITION DNA sequence.
CITBI-EI-2544A19.TF CITBI-EI Homo sapiens genomic clone 2544A19,
GSS.
ACCESSION AO390169
VERSION AO390169.1 GI:4361192
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Zhao, S., Adams, M. D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J. C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: CITBI-EI-2544A19.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source 1..418
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2544A19"
/clone_lib="CITBI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 132 a 109 c 104 g 73 t

ORIGIN

Query Match
Best Local Similarity 86.2%; Score 107.6; DB 17; Length 418;
Matches 119; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1 AGTACTCAGGAGGCTGAGACAGAAATCGCTTGAAACCGGAGGAGGAGGTTGCAGTG 60
|||||
Db 95 AGTCTGAGGAGGCTGAGGAGGAATCACTTGAAACCGGAGGAGGAGGTTGCAGTG 154
|||||

0Y 61 AGCCGAGATCAGCGCACTAGATTCATCCAGCTGGCGGAAGACAAGACTCCGTCTCA 120
|||||
Db 155 AGCCGAGATCAGCGCACTAGATTCATCCAGCTGGCGGAAGACAAGACTCCGTCTCA 214
0Y 121 AAAAAAAAAATCGTTACA 138
|||||
Db 215 AAAAAAAAAAACAAACA 232

RESULT 10
BMS09394 469 bp mRNA linear EST 15-FEB-2002
LOCUS 1h17f10.y1 Human Insulinoma Homo sapiens cDNA 5' similar to
DEFINITION SW:AU8.HUMAN P39195 ALU SUBFAMILY SX SEQUENCE CONTRAMINATION
WARNING ENTRY. [1] ; mRNA sequence.

ACCESSION BMS09394
VERSION BMS09394
KEYWORDS EST.
SOURCE BMS09394.1 GI:18680537
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 469)
AUTHORS Melton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hiller,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Riter,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@hbp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 416.

FEATURES
source location/Qualifiers
1..469
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human Insulinoma"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permut
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 149 a 93 c 94 g 133 t
ORIGIN

Query Match 6.1%; Score 107.2; DB 13; Length 469;
Best Local Similarity 81.6%; Pred. No. 8,6e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

0Y 1 ACCTACTCAGAGAGCTGAGACAGAGAAATCGTTGAACCCGGAGAGCAGAGTTGCAGTG 60
|||||
Db 285 AGCCACTCGGAGAGCTTAATGGAGAAATCGTTGAACCTGGAGCAGAGTTGCAGTG 344

0Y 61 AGCCGAGATCAGCGCACTAGATTCATCCAGCTGGCGGAAGACAAGACTCCGTCTCA 120
|||||
Db 345 AGCCGAGATCAGCGCACTAGATTCATCCAGCTGGCGGAAGACAAGACTCCGTCTCA 404
0Y 121 AAAAAAAAAATCGTTACATTTATGTGATTT 152
|||||
Db 405 AAAAAAAAAAGGTTGAAAAATGCTGCTTT 436

RESULT 11
B1468297 516 bp mRNA linear EST 11-MAR-2002
LOCUS 1d87b01.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE:5022649
DEFINITION 5', mRNA sequence.

ACCESSION B1468297
VERSION B1468297.1 GI:15284406
KEYWORDS EST.
SOURCE B1468297.1 GI:15284406
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 516)
AUTHORS Melton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hiller,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Riter,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@hbp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
High quality sequence stop: 457.

FEATURES
source location/Qualifiers
1..516
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5022649"
/clone_lib="Human Insulinoma"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permut
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 157 a 103 c 104 g 152 t
ORIGIN

Query Match 6.1%; Score 107.2; DB 13; Length 516;
Best Local Similarity 81.6%; Pred. No. 8,7e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

0Y 1 ACCTACTCAGAGAGCTGAGACAGAGAAATCGTTGAACCCGGAGAGCAGAGTTGCAGTG 60
|||||
Db 285 AGCCACTCGGAGAGCTTAATGGAGAAATCGTTGAACCTGGAGCAGAGTTGCAGTG 344


```

OY      61  AGCCGATCAGCCACTAGACCTCATCCAGCTGGGCGAAGACAGACTCCGTCTCA 120
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Db      345  AGCCAGGACGACGCGCTGACTCATTCACCTGGGTGACAGACAGACTCATCTCA 404
OY      121  AAAAAAAAAATCGTTACATTATGTGTGATT 152
        ||||| || || || || || || || || || || || || || || || ||
Db      405  AAAAAAAAAAGTTAGAAAAATGCTGCTTT 436

RESULT 12
LOCUS    BQ270800          529 bp      mRNA      linear      EST 07-MAY-2002
DEFINITION 1K05D06.Y1 Human insulinoma Homo sapiens cDNA clone IMAGE: 5779930
ACCESSION BQ270800
VERSION   BQ270800.1 GI:20495866
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 529)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
           Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
           Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
           Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
           M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
           Jackson,Y. and Bowers,Y.
           Endocrine Pancreas Consortium
           Unpublished (2000)
           Other-ESTs: 1K05D06.x1
           Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
           Endocrine Pancreas Consortium
           Harvard University, Howard Hughes Medical Institute
           Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
           MA 02138
           Tel: 617-495-1812
           Fax: 617-495-8557
           Email: dmelton@biohp.harvard.edu
           Library was constructed by Dr. J. Ferrer in vivo mass-excised to
           pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
           University Genome Sequencing Center for information on obtaining a
           clone please contact: Dr. Hiroshi Inoue (hinoue@lm.wustl.edu)
           Seq primer: -40RP from Gibco
           High quality sequence stop: 428.
           Location/Qualifiers
               1..529
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE: 5779930"
               /clone_lib="Human insulinoma"
               /tissue_type="Insulinoma"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
               XhoI; Site:2: EcoRI; Constructed with lambda ZapII system
               (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
               pBluescript SK- by Dr. H. Inoue following the Washington
               University protocol
               (http://genome.wustl.edu/est/lambda-protocol.shtml).
               Please contact Hiroshi Inoue, MD/PhD for further
               information on this library (Metabolism Division, Permutt
               Laboratory, Washington University School of Medicine, Box
               8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
               is a Washington University Pancreas EST project library."
BASE COUNT 160 a 107 c 107 g 155 t

ORIGIN
Query Match 6.1%; Score 107.2; DB 14; Length 529;
Best Local Similarity 81.6%; Pred. No. 8.7e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
OY      1  AGCTACTCAGGAGGCTGACACGAGATCGCTTGAACCCGGAGGACAGAGTTGCAGTG 60

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```

Db      285  AGCCACTGGGAGGCTTAAATGGAGAAATCGTTGAACCTGGAGGAGAGGTTGCAGTG 344
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      61  AGCCGATCAGCCACTAGACCTCATCCAGCTGGGCGAAGACAGACTCCGTCTCA 120
        ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      345  AGCCAGGACGACGCGCTGACTCATTCACCTGGGTGACAGACAGACTCATCTCA 404
OY      121  AAAAAAAAAATCGTTACATTATGTGTGATT 152
        ||||| || || || || || || || || || || || || || || || ||
Db      405  AAAAAAAAAAGTTAGAAAAATGCTGCTTT 436

RESULT 13
LOCUS    BQ267333          556 bp      mRNA      linear      EST 07-MAY-2002
DEFINITION 1K02C03.Y1 Human insulinoma Homo sapiens cDNA clone IMAGE: 5779589
ACCESSION BQ267333
VERSION   BQ267333.1 GI:20492398
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 556)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
           Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
           Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
           Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
           M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
           Jackson,Y. and Bowers,Y.
           Endocrine Pancreas Consortium
           Unpublished (2000)
           Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
           Endocrine Pancreas Consortium
           Harvard University, Howard Hughes Medical Institute
           Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
           MA 02138
           Tel: 617-495-1812
           Fax: 617-495-8557
           Email: dmelton@biohp.harvard.edu
           Library was constructed by Dr. J. Ferrer in vivo mass-excised to
           pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
           University Genome Sequencing Center for information on obtaining a
           clone please contact: Dr. Hiroshi Inoue (hinoue@lm.wustl.edu)
           Seq primer: -40RP from Gibco
           High quality sequence stop: 428.
           Location/Qualifiers
               1..556
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE: 5779589"
               /clone_lib="Human insulinoma"
               /tissue_type="Insulinoma"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
               XhoI; Site:2: EcoRI; Constructed with lambda ZapII system
               (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
               pBluescript SK- by Dr. H. Inoue following the Washington
               University protocol
               (http://genome.wustl.edu/est/lambda-protocol.shtml).
               Please contact Hiroshi Inoue, MD/PhD for further
               information on this library (Metabolism Division, Permutt
               Laboratory, Washington University School of Medicine, Box
               8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
               is a Washington University Pancreas EST project library."
BASE COUNT 167 a 112 c 113 g 164 t

ORIGIN
Query Match 6.1%; Score 107.2; DB 14; Length 556;
Best Local Similarity 81.6%; Pred. No. 8.8e-16;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```

Query Match	6.1%	Score 107.2	DB 14	Length 589
Best Local Similarity	81.6%	Pred. No. 8.8e-16		
Matches 124; Conservative	0	Mismatches 28	Indels 0	Gaps 0

OY 121 AAAAAAAAAATCGTTACAAT-----TTAAGTGCTGATTACCCCTTTTTACTCATCA 175
 | | | | | | | | | | | | | | | | | |
Db 427 AAAAAAAAAAAAAAATTCGACTTTAACTGTACTACTCACCACGGTAGATAGCAA 480

Qy 176 AGACAGCAGCTACTTTAAAGCAAGTCATGATTTGAAGCCTTCTTCCATATAAA 235
 Db 487 ACTAGCAGGAGTAACTTAATTGATTTACCAAGTAAATTTGATTAATA 546
 Qy 236 GGGAGATT 243
 Db 547 TAGACAGT 554

Search completed: December 19, 2002, 14:46:57
 Job time : 2153 secs

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